

Landisman  
09/16/2006  
08/30/5518  
Seg-ID7

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2002, 19:59:38 ; Search time 2327.3 Seconds  
(without alignments)  
11412.563 Million cell updates/sec

Title: US-08-305-518-7

Perfect score: 1610  
Sequence: 1 CGGATGACCTCTGTGAACCT.....GCTCTGCACATTAGAGCCG 1610

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID         | Description         |
|------------|--------|-------------|--------|----|------------|---------------------|
| 1          | 1610   | 100.0       | 1610   | 6  | ARI06017   | ARI06017 Sequence   |
| 2          | 1610   | 100.0       | 1610   | 6  | HUMOPTOIDA | L29301 Homo sapien  |
| 3          | 1562.6 | 97.1        | 2162   | 6  | A87781     | A87781 Sequence 7   |
| 4          | 1553   | 96.5        | 2162   | 9  | HUMWORTX   | L25119 Human Mu op  |
| 5          | 1346.2 | 83.6        | 1473   | 9  | HSU012569  | U12569 Human mu op  |
| 6          | 1329.8 | 82.6        | 1399   | 9  | AY038989   | AY038989 Macaca fa  |
| 7          | 1258   | 78.1        | 1881   | 4  | PICMUOPR   | L38645 Sus scrofa   |
| 8          | 1167.8 | 72.5        | 1303   | 9  | AF286024   | AF286024 Macaca mu  |
| 9          | 1139.6 | 70.8        | 1415   | 4  | BT089677   | U89677 Bos taurus   |
| 10         | 1123.8 | 69.8        | 1618   | 6  | ARI06013   | ARI06013 Sequence   |
| 11         | 1123.8 | 69.8        | 1618   | 6  | ARI06014   | ARI06014 Sequence   |
| 12         | 1123.8 | 69.8        | 1618   | 6  | ARI53354   | ARI53354 Sequence   |
| 13         | 1123.8 | 69.8        | 1618   | 6  | ARI53355   | ARI53355 Sequence   |
| 14         | 1122   | 69.7        | 2229   | 6  | A68824     | A68824 Sequence 1   |
| 15         | 1122   | 69.7        | 2229   | 10 | MMU019380  | U19380 Mus musculu  |
| 16         | 1120.8 | 69.6        | 1586   | 10 | RATMORA    | L13069 Rattus norv  |
| 17         | 1110.4 | 69.0        | 1610   | 10 | MMU026915  | U26915 Mus musculu  |
| 18         | 1103   | 68.5        | 2397   | 10 | RATROBR    | D16349 Rat mRNA fo  |
| 19         | 1064.6 | 66.1        | 1448   | 10 | RNU02083   | U02083 Rattus norv  |
| 20         | 1039   | 64.5        | 1401   | 10 | RATMOPROD  | L22455 Rat mu opio  |
| 21         | 1031.6 | 64.1        | 2135   | 6  | ARI48257   | ARI48257 Sequence   |
| 22         | 1031.6 | 64.1        | 2135   | 10 | RATMOPROA  | L20684 Rattus norv  |
| 23         | 1026.2 | 63.7        | 1367   | 10 | RNU35424   | U35424 Rattus norv  |
| 24         | 930    | 57.8        | 1543   | 10 | AF074974   | AF074974 Mus muscu  |
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| 27         | 924    | 57.4        | 1729   | 10 | AF167568   | AF167568 Mus muscu  |
| 28         | 572.8  | 35.6        | 720    | 10 | S77863     | S77863 mu-opioid r  |
| 29         | 555.4  | 34.5        | 1387   | 5  | AF132813   | AF132813 Danilo rer |
| 30         | 553.2  | 34.4        | 1231   | 5  | CCMUOPI    | Y10904 C. commerson |
| 31         | 526.4  | 32.7        | 96310  | 9  | ALI36444   | ALI36444 Human DNA  |
| 32         | 517    | 32.1        | 182048 | 2  | AC027439   | AC027439 Homo sapi  |
| 33         | 487.4  | 30.3        | 182383 | 2  | AC021745   | AC021745 Homo sapi  |
| 34         | 487.4  | 30.3        | 1598   | 9  | HSOPRM12   | AF024516 Homo sapi  |
| 35         | 454.6  | 28.2        | 1418   | 10 | RATROBR    | U00475 Rattus norv  |
| 36         | 454.6  | 28.2        | 1418   | 10 | HSU07882   | D16348 Rat mRNA fo  |
| 37         | 444    | 27.6        | 1773   | 9  | HSU10504   | U07882 Human delta  |
| 38         | 443.2  | 27.5        | 1136   | 6  | HSU08615   | U10504 Human delta  |
| 39         | 443.2  | 27.5        | 1629   | 6  | AR086615   | AR086615 Sequence   |
| 40         | 443.2  | 27.5        | 1834   | 10 | S65335     | S65335 delta opioi  |
| 41         | 443.2  | 27.5        | 1835   | 10 | MUSDOFRCP  | L07271 Mouse delta  |
| 42         | 443.2  | 27.5        | 2203   | 10 | S66181     | S66181 delta opiat  |
| 43         | 443.2  | 27.5        | 2218   | 6  | A68826     | A68826 Sequence 3   |
| 44         | 443.2  | 27.5        | 2219   | 6  | A38528     | A38528 Sequence 1   |
| 45         | 443.2  | 27.5        | 2219   | 10 | MUSDELTO   | L06322 Mus musculu  |

## ALIGNMENTS

| RESULT | LOCUS    | DEFINITION                         | ACCESSION | VERSION    | KEYWORDS    | SOURCE   | ORGANISM | REFERENCE           | AUTHORS | JOURNAL                                    | FEATURES                            | BASE COUNT | ORIGIN            |
|--------|----------|------------------------------------|-----------|------------|-------------|----------|----------|---------------------|---------|--|-------------------------------------|------------|-------------------|
| 1      | ARI06017 | Sequence 7 from patent US 6103492. | ARI06017  | ARI06017.1 | GI:12820082 | Unknown. | Unknown. | 1 (bases 1 to 1610) | Yu, L.  | Polynucleotide encoding mu opioid receptor | Patent: US 6103492-A 7 15-AUG-2000; | 384 a      | 467 c 359 g 400 t |

Query Match 100.0%; Score 1610; DB 6; Length 1610;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 ATGCTCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
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QY 961 CGCCTTCATTATGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
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QY 1561 CATCAACCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1610
DB 1561 CATCAACCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1610

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## RESULT 2

HUMOPIODA 1610 bp mRNA PRI 03-AUG-1995  
 LOCUS HUMOPIODA  
 DEFINITION Homo sapiens oploid receptor mRNA, complete cds.  
 ACCESSION 129301  
 VERSION 129301.1 GI:459831  
 KEYWORDS oploid receptor.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1610)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Westek,A., Hurley,J.H., Bye,L.S., Campbell,A.D., Chen,X., Tian,M.,  
 Liu,J., Schulman,H. and Yu,L.  
 The human mu oploid receptor: modulation of functional  
 desensitization by calcium/calmodulin-dependent protein kinase and  
 protein kinase C

J. Neurosci. 15 (3), 2396-2406 (1995)  
 MEDLINE 95198115

## FEATURES

## source

Location/Qualifiers  
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| QY         | 901  | AACATTCCTCATCCACCAACCTGGATAGTGGAAAAACCTGCTGAAGATCTGTTTTCATCTT  | 960                  |
| Db         | 901  | AACATTCCTCATCCACCAACCTGGATAGTGGAAAAACCTGCTGAAGATCTGTTTTCATCTT  | 960                  |
| QY         | 961  | CGCCTTATTAATGCCAGTGTCTCATATACCGTGTGCTATGGACATGATATCTTGCGCCT    | 1020                 |
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| QY         | 1021   | CAAGATGTCGCAATGCTCTCTGGCTCCAAAGAAAGACAGAAATCTTTCGAAGATATAC     | 1080                 |
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| QY         | 1081   | CAGATGCTGCTGGTGGTGGCTGTGTTATATCGTCTGGACTCCCATTCACATTTTA        | 1140                 |
| Db         | 1081   | CAGATGCTGCTGGTGGTGGCTGTGTTATATCGTCTGGACTCCCATTCACATTTTA        | 1140                 |
| QY         | 1141   | CGTCATCATTAAGACCTTGGTTACATCCACAAATACGTTCCAGACTGTTCTTGGCA       | 1200                 |
| Db         | 1141   | CGTCATCATTAAGACCTTGGTTACATCCACAAATACGTTCCAGACTGTTCTTGGCA       | 1200                 |
| QY         | 1201   | CTTCTGCATTTGCTCTAGGTTACACAAACAGCTGCTCAACCCAGTCTTATATGCAATTTCT  | 1260                 |
| Db         | 1201   | CTTCTGCATTTGCTCTAGGTTACACAAACAGCTGCTCAACCCAGTCTTATGCAATTTCT    | 1260                 |
| QY         | 1261   | GGATGAAACACTCCAAAGATGCTTCAGAGAGTTCTGATATCCCACTCTTCCACATTTGA    | 1320                 |
| Db         | 1261   | GGATGAAACACTCCAAAGATGCTTCAGAGAGTTCTGATATCCCACTCTTCCACATTTGA    | 1320                 |
| QY         | 1321   | GCACAAACACTCCACTGGAATTCGTAGAGAACACTAGAGACACCCCTCCACGGCAATAC    | 1380                 |
| Db         | 1321   | GCACAAACACTCCACTGGAATTCGTAGAGAACACTAGAGACACCCCTCCACGGCAATAC    | 1380                 |
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| QY         | 1561   | CATCCAACCTCTTCTCTGTGGCCACTGTGCTCTGCACATTAGAGGCGG               | 1610                 |
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| LOCUS      | A87781   | 2162 bp  | DNA                  |
| DEFINITION | Sequence 7 from Patent WO9833937.  |  |                      |
| ACCESSION  | A87781   |  |                      |
| VERSION    | A87781.1   | GI:6736383   |                      |
| KEYWORDS   |  |  |                      |
| SOURCE     | unidentified.  |  |                      |
| ORGANISM   | unclassified.  |  |                      |
| REFERENCE  | 1 (bases 1 to 2162)  |  |                      |
| AUTHORS    | Hoehle,M. and Wendel,B.  |  |                      |
| TITLE      | GENOMIC SEQUENCE OF THE HUMAN mu -OPIOID RECEPTOR GENE AND THE VARIANTS, POLYMORPHISMS AND MUTATIONS THEREOF |  |                      |
| JOURNAL    | Patent: WO 9833937-A 7 06-AUG-1998;  |  |                      |
| FEATURES   | HOEHLE MARGRET (DE); WENDEL BIRGIT (DE)  |  |                      |
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## ORIGIN

Query Match 97.1%; Score 1562.6; DB 6; Length 2162;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1576; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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| QY         | 935   | CTGCTGGAAGTACGTGTGTTTTCATCTTCGCTTCATATATCCAGTGCCTATCATATTCGCTG  | 994         |
| Db         | 909   | CTGCTGGAAGTACGTGTGTTTTCATCTTCGCTTCATATATCCAGTGCCTATCATATTCGCTG  | 968         |
| QY         | 995   | TGCTATGAGCTGATGATCTGGCCCTCAAGAGTGTCCGATCCTCTGCGCTCCAAAGAA       | 1054        |
| Db         | 969   | TGCTATGAGCTGATGATCTGGCCCTCAAGAGTGTCCGATCCTCTGCGCTCCAAAGAA       | 1028        |
| QY         | 1055  | AAGGACAGGAATCTTCGAAGATCCACAGAGTGTGCTGTGTGTGTGTGTGTGTTATC        | 1114        |
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| QY         | 1235  | CTCAACCCAGTCCCTTATATGCAATTTCTGATGAAACCTTCAACGATCCTTCAGAGATTG    | 1294        |
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| QY         | 1355  | AGAACCCACCCCTCCACAGGCAATACAGTATAGTAACATCATCAGCTAGAAAAATCTG      | 1414        |
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| QY         | 1415  | GAAGCAGAAACCTGCTCCGTTGCCCTTAACAGAGGCTCTCATGCCATTCGACCTTCACCAAGC | 1474        |
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| DEFINITION | Human mu opioid receptor variant (MOR1) mRNA, complete cds.   |   |             |
| ACCESSION  | U12569  |   |             |
| VERSION    | U12569.1  | GI:607911   |             |
| KEYWORDS   |   |   |             |
| SOURCE     | human.  |   |             |
| ORGANISM   | Homo sapiens  |   |             |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |   |             |
| AUTHORS    | 1 (bases 1 to 1473)   |   |             |
| TITLE      | Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH cells and human brain                            |   |             |
| JOURNAL    | FEBS Lett. 354 (2), 213-216 (1994)  |   |             |
| MEDLINE    | 95046336  |   |             |
| REFERENCE  | 2 (bases 1 to 1360)   |   |             |
| AUTHORS    | Wang, J.B., Johnson, P.S., Persico, A.M., Hawkins, A.L., Griffin, C.A.  |   |             |

TITLE Human mu opiate receptor. cDNA and genomic clones, pharmacologic characterization and chromosomal assignment  
JOURNAL FEBS Lett. 338 (2), 217-222 (1994)  
MEDLINE 94139928  
REFERENCE 3 (bases 1 to 1473)  
AUTHORS Bare, L.A.  
TITLE Direct Submission  
JOURNAL Submitted (24-JUL-1994) Lance A. Bare, Ohmeda, PPD, 100 Mountain Avenue, Murray Hill, NJ 07974, USA

FEATURES  
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1. 1473  
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RESULT 6  
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 LOCUS Macaca fascicularis mu-opioid receptor mRNA, complete cds.  
 DEFINITION AY038989  
 ACCESSION AY038989.1 GI:14718771  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Macaca fascicularis.  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 Cercopithecoidea; Macaca.  
 1 (bases 1 to 1399)  
 Miller, G.M. and Madras, B.K.  
 Cloning of the Macaca fascicularis mu opioid receptor  
 2 (bases 1 to 1399)  
 Miller, G.M. and Madras, B.K.  
 Direct Submission  
 Submitted (07-JUN-2001) Neurochemistry, New England Primate  
 Research Center, Harvard Medical School, One Pine Hill Drive,  
 Southborough, MA 01772, USA  
 Location/Qualifiers  
 1. 1399  
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QY 282 ATGCCCTTGGGAGTACCAAGTTGCTCCCGAGCACACCGCCGGTTCCTGGTCAACTGT 341  
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| OY                         | 1422 | AAACTGTCCGCTTGCCCTAACAGGGCTCATGCCATTCCGACCTTCACCAAGCTTAGAAG       | 1481   |             |
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| OY                         | 1482 | CCACCATCATGTATGGAGAAGAGTGTCTTCCAAGATGTAGAGAGGCTCTAATTCCTAG        | 1541   |             |
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| LOCUS                      |      | Sus scrofa mu opioid receptor mRNA, complete cds.                 | MAM  | 03-MAR-1999 |
| DEFINITION                 |      | L38645  |  |             |
| ACCESSION                  |      | L38645.1  |  |             |
| VERSION                    |      | GI:2072391  |  |             |
| KEYWORDS                   |      | .   |  |             |
| SOURCE                     |      | pig.  |  |             |
| ORGANISM                   |      | Sus scrofa  |  |             |
| REFERENCE                  |      | Euarivota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |  |             |
| AUTHORS                    |      | Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.                 |  |             |
| TITLE                      |      | 1 (bases 1 to 1881)   |  |             |
| JOURNAL                    |      | Pampusch,M.S., Osinski,M.A., Brown,D.R. and Murlough,M.P.         |  |             |
| MEDLINE                    |      | The porcine mu opioid receptor: molecular cloning and mRNA        |  |             |
| REFERENCE                  |      | distribution in lymphoid tissues                                  |  |             |
| AUTHORS                    |      | J. Neuroimmunol. 90 (2), 192-198 (1998)                           |  |             |
| TITLE                      |      | 2 (bases 1 to 1881)   |  |             |
| JOURNAL                    |      | Osinski,M.A.  |  |             |
| MEDLINE                    |      | Direct Submission   |  |             |
| REFERENCE                  |      | Submitted (19-SEP-1996) Mark A. Osinski, Veterinary Pathobiology, |  |             |
| AUTHORS                    |      | University of Minnesota, St. Paul, MN 55108, USA                  |  |             |
| TITLE                      |      | On May 6, 1997 this sequence version replaced gi:1553056.         |  |             |
| JOURNAL                    |      | Location/Qualifiers   |  |             |
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|                            |      | LCHSVRYIAVGVHPVKALDERPRRNKKTIIVCWMLISAIGLPVMMATTKYNGSG            |  |             |
|                            |      | DCALTFSHPHTWMENLIKICVFIFAIPIMPVLIIIVCGIMLTIKSRPMISGSEKRP          |  |             |
|                            |      | NLRRTTRNVLYVAVFYVCYTPPHIHVIYIKALITIIPETTESVWHCIAGTYNSCL           |  |             |
|                            |      | NPVLFARLEDFEKFRCFRFCIPTSTIEOONSARIKONTRDHPSTANTVDFTNHOLE          |  |             |
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| ORIGIN                     |      | 462 t   |  |             |
| Query Match                |      | 76.1%; Score 1258; DB 4; Length 1881;                             |  |             |
| Best Local Similarity      |      | 88.4%; Pred. No. 0;   |  |             |
| Matches 1425; Conservative |      | 0; Mismatches 175; Indels 12; Gaps 5;                             |  |             |
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| OY                         | 64   | CTCAGCTCGTGCCTCCGCTGACGCTCTCTGTGCTCAGCCAGGACGTGTTCTGTA            | 123  |             |

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| O | y | .124 | A G A A A C A G C A G A G A C C T T G S C A G O G G G A A A G A A G A G C G G C T T G A G C G C T T T G A A C C C G A A | 183   |     |
| D | b | 118  | A G A A G T A G A C A G A C C C T G C G G G G C C T G A G A G A M A C G G C T G A G C G C C T G A M A C C C G A         | 177   |     |
| O | y | 184  | A A G T C T G S G T C T C T T G S G T A C C T C G A C A G S G T G S C --- G C C G G G C G T C A G A C C A               | 239   |     |
| D | b | 178  | A A G C C C G G G T G A T G C C G G T T A C C T C A T G C T G T G C C A C C G C C C A G C C T G A G A C C A             | 237   |     |
| O | y | 240  | T G S A C A G A C G A G C G T G C C C C C A G A A C C C A G A C A T T G A C T A G T A G C T T --- G G C T A C T         | 296   |     |
| D | b | 238  | T G S A C A G A G A G G C T G A C C C C C G A A A G C C A G A A T T G A C T G A T C C C T T C T G C C C T Y T           | 297   |     |
| O | y | 297  | C A A G T T G C T C C C A G A C C C A G C C C C G G T T C T T G S G T C A A C T T G T C C A C T T A G A T G G C A       | 356   |     |
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| O | y | 417  | C T C G C A C C G S G A G T C E C T C A T A T C A C G C C A T C A G A T C A T G C C C T A C T C A T C A G               | 476   |     |
| D | b | 418  | C T C G C A C C G S G A G T C C T T C C A T G G T A C G C C A T C A C A T A T G G C C C T C T A C T C A T C A G         | 477   |     |
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| O | y | 597  | C C A T A C C C T G C C C C T T C A A G T G A T T A C T A N T G S A A C A T N S G C A T T T T G S A C C A               | 656   |     |
| D | b | 598  | C C A G T A C C T G C C C C T T C A A G T G C A T T A C T A A T N G S A A G T G S C C G T T T G A A C C A               | 657   |     |
| O | y | 657  | T C C T T T G C A A G A T A G T A T C C A T A G A T T A C T A A C A T G T T C A C A C A C A T A T T C A C C             | 716   |     |
| D | b | 658  | T C C T C T C A A A G A T G T A T C C A T A G A T F A C T A C A A T N G T T C A C A C A C A T A T T C A C C             | 717   |     |
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| O | y | 897  | C A C T A A C A T T C T C A T C C A A C C T G S A A G G A A A A C C T G S A A G A A T C T G T T T T C A                 | 956   |     |
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ACCESSION AF286024.1 GI:9664878  
VERSION  
KEYWORDS  
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ORGANISM Macaca mulatta  
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Cercopitheciinae; Macaca.  
REFERENCE 1 (bases 1 to 1203)  
AUTHORS Miller, G.M. and Madras, B.K.  
JOURNAL Cloning of the Macaca mulatta mu opioid receptor  
TITLE Unpublished  
REFERENCE 2 (bases 1 to 1203)  
AUTHORS Miller, G.M. and Madras, B.K.  
JOURNAL Direct Submission  
TITLE Submitted (11-JUL-2000) Neurochemistry, New England Regional  
JOURNAL Primate Research Center, Harvard Medical School, One Pine Hill  
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BASE COUNT 299 a 350 c 242 g 312 t  
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Db

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 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1618)  
 AUTHORS Yu, L.  
 TITLE Polynucleotide encoding mu opioid receptor  
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ACCESSION ARI06014  
VERSION ARI06014.1 GI:12820079  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1618)  
AUTHORS Yu, L.  
TITLE Polynucleotide encoding mu opioid receptor  
JOURNAL Patent: US 6103492-A 3 15-AUG-2000;  
FEATURES  
source location/qualifiers  
BASE COUNT 390 a 486 c 370 g 372 t  
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Query Match 69.8%; Score 1123.8; DB 6; Length 1618;  
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Db 1435 TCCTTAACCTTAGAGGCGGCATCTAGCTGATTCAGATTCAGGCTGTGGAG 1494  
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RESULT 12

AR153354

LOCUS AR153354 1618 bp DNA PAT 08-AUG-2001

DEFINITION Sequence 1 from patent US 6235496.

ACCESSION AR153354

VERSION AR153354.1 GI:15120886

KEYWORDS

SOURCE

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 1618)

TITLE Yu, L.

JOURNAL Nucleic acid encoding mammalian mu opioid receptor

FEATURES Patent: US 6235496-A 1 22-MAY-2001.

source Location/Qualifiers

1. 1618

/organism="unknown"

BASE COUNT 390 a 486 c 370 g 372 t

ORIGIN

Query Match 69.8%; Score 1123.8; DB 6; Length 1618;

Best Local Similarity 83.7%; Pred. No. 2e-287;

Matches 1323; Conservative 0; Mismatches 247; Indels 11; Gaps 4;

27 GTGGAGAGGGGCTATACGCAGAGAGATGTCAAGTGTCTGAGTCCCTCCGCTG 86

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QY 446 GCCATCAGATGAG 505

Db 415 GCCATCAGATGAG 474

QY 506 CTGTGTATGTATGT 565

Db 475 CTGTGTATGTATGT 534

QY 566 TTCAACCTGT 625

Db 535 TTCAACCTGT 594

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QY 1286 AGAGATTTGT 1345

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Db 1315 CAGAACCTAG 1374

QY 1406 GAAATCTGGAAG 1465

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RESULT 13

AR153355

LOCUS AR153355 1618 bp DNA PAT 08-AUG-2001

DEFINITION Sequence 3 from patent US 6235496.

ACCESSION AR153355

VERSION AR153355.1 GI:15120887

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.  
1 (bases 1 to 1618)

REFERENCE

1 (bases 1 to 1618)

YU, L.

Nucleic acid encoding mammalian mu opioid receptor

JOURNAL Patent: US 6235496-A 3 22-MAY-2001;

FEATURES

Location/Qualifiers

source

1..1618

/organism="unknown"

BASE COUNT 390 a 486 c 370 g 372 t

ORIGIN

Query Match

69.8%; Score 1133.8; DB 6; Length 1618;

Best Local Similarity 83.7%; Pred. No. 2e-287;

Matches 1323; Conservative 0; Mismatches 247; Indels 11; Gaps 4;

27 GTGGAGGGGGCTATACGAGAGAGAGATGTGAGATGCTAGCTGCGTCCCTCCGCTG 86  
 2 GTGGAGGGGGCTATACGAGAGAGAGATGTGAGATGCTAGCTGCGTCCCTCCGCTG 60  
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 ACCESSION A68824  
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 ORGANISM unidentified.  
 REFERENCE 1 (bases 1 to 2229)  
 AUTHORS Kieffer, B. L., Mathes, H. W., Simonin, F. H., Dietrich, A. and Lemmeur, M.  
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 JOURNAL PATENT: WO 9802534-A 1 22-JAN-1998;  
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BASE COUNT 562 a 608 c 489 g 570 t

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Query Match 69.7%; Score 1122; DB 6; Length 2229;  
 Best local Similarity 83.4%; Pred. No. 6.2e-287;  
 Matches 1324; Conservative 0; Mismatches 255; Indels 9; Gaps 4;

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 VERSION U19380.1 GI:885864  
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 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 2229)  
 AUTHORS Kaufman,D.L., Keith,D.E., Anton,B., Tian,J., Magendzo,K.,  
 Newman,D., Tran,T., Lee,D.S., Wen,C., Xia,Y., Lusis,A.J. and  
 Evans,C.J.  
 TITLE Characterization of the murine mu opioid receptor gene

JOURNAL J Biol. Chem. 270 (26), 15877-15883 (1995)  
MEDLINE 95318184  
REFERENCE 2 (bases 1 to 2229)  
AUTHORS Evans, C.C.  
TITLE Direct Submission  
JOURNAL Submitted (04-JAN-1995) Christopher J Evans, Psychiatry and  
Biobehavioral Sciences, University of California at Los Angeles,  
UCLA-NPI, 760 Westwood Plaza, Los Angeles, CA 90024-1759, USA

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## CDS

BASE COUNT 562 a 608 c 489 g 570 t  
ORIGIN

Query Match 69.7%; Score 1122; DB 10; Length 2229;  
Best Local Similarity 83.4%; Pred. No. 6, 2e-287;  
Matches 1324; Conservative 0; Mismatches 255; Indels 9; Gaps 4;

QY 4 ATGAGCCTGTGTGACTAAGTGTGGAGGGGCTATACGACAGAGAGAAATGTAGATG 63  
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QY 64 CTCAGCTGGGTCCTCCGCTGACGCTCCCTGTCTGTCAGCGAGGACGTTCGTGTA 123  
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• Thu May 2 11:42:20 2002

us-08-305-518-7.rge

Page 17

Search completed: May 1, 2002, 22:13:58  
Job time: 8060 sec

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PT related vectors, transformed cells, antibodies etc., useful in  
PT diagnosis, treatment and drug screening.

XX Claim 5: Page 208-210; 266pp: English.

XX A cDNA library constructed from human caudate nucleus mRNA was  
CC screened with rat mu opiod receptor cDNA under conditions of  
CC low stringency. One positive clone included the sequence given in  
CC AA089226, encoding a mu opiod receptor MOR (AAR71964). The cDNA  
CC is used for prodn. of recombinant MOR, in gene therapy, etc.  
XX

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DB 181 gaaagcttcgtgtcctgcttacctgcacagcggtgcccgccgctcagtaacct 240  
QY 241 GGACAGAGCGTGGTCCCGCCGAGAACGCGACCAATTTGACATGATGCTTGGCGTCAAG 300  
DB 241 ggacagagcggtggctcccgagaaacgacccaatttgacatgatgcttggcgctcaag 300  
QY 301 TTGCTCTCCAGCAGCAGCCCGGTTCTTGCTGATGATGATGATGATGATGATGAT 360  
DB 301 ttgctctccagcagcagcccggttcttgctgatgatgatgatgatgatgatgat 360  
QY 361 GTCCGACCATGCGGTCCGAAACCGACCGACCTGGCGGAGAGACAGCTGTGCCCTCC 420  
DB 361 gtccgacctgctgtccgaaacgacccgacccgttcttgctgatgatgatgatgatgat 420  
QY 421 GACCGGAGTCCCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
DB 421 gaccggagtcctcccatgatgatgatgatgatgatgatgatgatgatgatgatgat 480  
QY 481 CGTGTGGGGCTCTTGGAACCTTCTGATGATGATGATGATGATGATGATGATGATGAT 540  
DB 481 cgtgtgggctcttggaaaccttctgatgatgatgatgatgatgatgatgatgatgat 540  
QY 541 GAAAGCTGCGCAGCAATCTTACATTTTCAACCTTGTCTGTGGAGATGCTTACCGACAG 600  
DB 541 gaaagctgcgccagcaaatcttaccttttcaaccttgtctgtggagatgctttaccgacag 600  
QY 601 TACCCTGCGCTCCAGAGTGTGATTAACATGGGAAATGGCAATTTGGAACCAATCT 660  
DB 601 taccctgcgctccagagtgtgattacctaagggaacatggcatttgaacacacct 660  
QY 661 TTGCAAGATAGTATCTCCATAGATTACTATTAACATGTTACACAGCATATTTCAACCTCTG 720  
DB 661 ttgcaagatagtatctccatagattactataacatgtttaccagcatatctacctctg 720  
QY 721 CACCATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
DB 721 caccatgagtgtgattgattgattgattgattgattgattgattgattgattgattgatt 780  
QY 781 TACTCCCGGAATGCAAAATTAATCAATGTCCTCAATGATGATGATGATGATGATGATGAT 840  
DB 781 tactcccggaatgcaaaatataatcaatgtctgaactgattcctctcagccatttg 840

QY 841 TCTTCTGTAATGTCATGCTGACAAACAAATACAGCAAGGTTCATGATGATGATGATGATGAT 900  
DB 841 tcttctgtaatgtcatgtctgacaaacaaatatacaggaagttcattagattgatactact 900  
QY 901 AACATTTCTCATCATCACTGCTACTGGGAAACCTGCTGAAGATCTGTGTTTCTTCTT 960  
DB 901 aacatttctcatcatcaactgctactgggaaacctgctgaagatctgtgtttcttctt 960  
QY 961 CGCCTTCATTAATGACAGTGTCTATTAACCGTGTGCTGATGATGATGATGATGATGATGAT 1020  
DB 961 cgccttcattaatgacagtgtctatataacggtgtgctgatgatgatgatgatgatgat 1020  
QY 1021 CAAGAGTTCGCCGATCTCTGCTGCAAAAGAAAGAGCAGAGATCTTGAAGATGAC 1080  
DB 1021 caagagtgtccgatctctctgctcgaagaaagagcagagatcttcgaagatgac 1080  
QY 1081 CAGGATGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1140  
DB 1081 caggatgctgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgtgctgt 1140  
QY 1141 CGTCATCATTAAGCCTTGTGTTACATCCAGAACTTACGTTCCAGACTGTTTCTTGCGCA 1200  
DB 1141 cgtcacatlaaagccttgtgttacatccagaaacttacgttccagactgtttcttgcgca 1200  
QY 1201 CTTCGATTTGCTCTAGTTTACAAACAGCTGCTCAACCCAGTCTTTATGATTTCT 1260  
DB 1201 cttcgatgttctctagtttacaacacagctgctccacccagctcttcttcttcttct 1260  
QY 1261 GGATGAAACTTCAACGATGCTTTCAGAGAGTTCTGTATGCCACTCTTCCAACTTTTA 1320  
DB 1261 ggatgaaacttcaacgatgctttcagagagttctgtatgccactcttccaacttga 1320  
QY 1321 GCACAAACTCCACTCGAATTCGTGAGAACTAGACACACCCCTCCAGGACCAATTC 1380  
DB 1321 gcacaaactccactcgaatttcgtgagaaactagacacacccctccaggaaccaattc 1380  
QY 1381 AGTGTAGTAATCATCATGCTAGTAAATCTGGAAGCAGAAATGCTCCGTTGCCCTTA 1440  
DB 1381 agtgtagtaatcatcatgctagtaaatctggaagcagaaatgctccggttgccctta 1440  
QY 1441 ACAGGCTTCATGCTTCCTGACCTTCACCAAGCTTGAAGCCACCATATATGTGGAAC 1500  
DB 1441 acaggcttcattgcttcctgaccttcaccaagcttgaagccacatatgttggaac 1500  
QY 1501 AGGTGCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
DB 1501 aggtgcttcaagatgatgatgatgatgatgatgatgatgatgatgatgatgatgat 1560  
QY 1561 CATCAACCTCTTCTCTGCGCACTGCTCTGACATTAGAGCCG 1610  
DB 1561 catcaaccttctctctgcgcactgctctgacatttagagccg 1610

RESULT 2  
AAA59503  
ID AAA59503 standard; cDNA; 1610 BP.  
XX  
AC AAA59503;  
XX  
DT 14-NOV-2000 (first entry)  
XX  
DE cDNA encoding a human mu opiod receptor polypeptide.  
XX  
KW mu opiod receptor; transcription regulatory polypeptide;  
KW opiod receptor-like polypeptide; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 239..1441  
FT /tag= a "mu opiod receptor"  
FT /product= "mu opiod receptor"



|        |   |  |      |
|--------|---|--|------|
| Oy     | 1561  | CACCAACGCTTTTCCHTGTGGCAGCTCGGCATTAAGAGGCCG     | 1610 |
| Xx     |   |  |      |
| Dd     | 1561  | cattcaacctcttcctcctgtgccaactgcgtgcacatlagagccg | 1610 |
|        |   |  |      |
| RESULT | 3   |  |      |
| ID     | AAV61984  |  |      |
| XX     | AAV61984  | standard; cDNA; 2162 BP.                       |      |
| AC     |   |  |      |
| XX     |   |  |      |
| DT     | 11-JAN-1999   | (first entry)                                  |      |
| XX     |   |  |      |
| DE     | Human mu-opioid receptor cDNA.  |  |      |
| XX     |   |  |      |
| KW     | Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;    |  |      |
| RW     | predisposition; addiction; analgesic; anaesthetic; anti-addictive;        |  |      |
| KM     | psychopharmaceutical agent; diagnostic; side effect; drug; opiate;        |  |      |
| KM     | cocaine; inherited alcoholism; human; ss.                                 |  |      |
| XX     |   |  |      |
| OS     | Homo sapiens.   |  |      |
| XX     |   |  |      |
| FH     | Key   | Location/Qualifiers                            |      |
| FT     | CDS   | 213..2040                                      |      |
| FT     |   | /tag= a  |      |
| FT     |   | /product= "mu-opioid receptor"                 |      |
| FT     | misc_feature  | 502..503                                       |      |
| FT     |   | /tag= b  |      |
| FT     | misc_feature  | /note= "Site of Intron 1"                      |      |
| FT     |   | 855..856                                       |      |
| FT     |   | /tag= c  |      |
| FT     | misc_feature  | /note= "Site of Intron 2"                      |      |
| FT     |   | 1376..1377                                     |      |
| FT     |   | /tag= d  |      |
| FT     |   | /note= "Site of Intron 3"                      |      |
| XX     |   |  |      |
| PN     | MO983J937-A2.   |  |      |
| PD     |   |  |      |
| XX     | 06-AUG-1998.  |  |      |
| XX     |   |  |      |
| PF     | 02-FEB-1998;  | 98MO-DE00382.                                  |      |
| XX     |   |  |      |
| PR     | 03-FEB-1997;  | 97DE-1003925.                                  |      |
| XX     |   |  |      |
| PA     | (DELB-) DELBRUECK CENT MOLECULARE MEDIZIN MAX.                            |  |      |
| PI     |   |  |      |
| PI     | Hoehe M, Wendel B:  |  |      |
| DR     | WPI; 1998-437487/37.  |  |      |
| XX     |   |  |      |
| PT     | New genomic and cDNA sequences encoding human mu-opioid receptor -        |  |      |
| PT     | used, e.g. to predict pre-disposition to addiction and for                |  |      |
| PT     | development of analgesics, anaesthetics and anti-addiction agents         |  |      |
| PS     |   |  |      |
| XX     |   |  |      |
| CC     | Claim 8; Page 14-15; 26pp; German.  |  |      |
| CC     | This sequence encodes a novel human mu-opioid receptor. This sequence and |  |      |
| CC     | its variants, polymorphisms and mutants are used in a method for          |  |      |
| CC     | detecting predisposition to disease, particularly addictive disease, by   |  |      |
| CC     | isolating DNA from a sample, genotyping selected positions and comparing  |  |      |
| CC     | with a reference DNA. Such sequences are used to develop analgesic,       |  |      |
| CC     | anaesthetic, anti-addictive and psychopharmaceutical agents, to construct |  |      |
| CC     | genes and vectors, particularly for pharmaceutical development, to        |  |      |
| CC     | develop diagnostic kits for predicting risk of addiction, response to     |  |      |
| CC     | analgesics or anaesthetics, or development of side effects from a drug.   |  |      |
| CC     | Particular applications are to determine risk of addiction to opiates or  |  |      |
| CC     | cocaine, or of developing inherited alcoholism.                           |  |      |
| XX     |   |  |      |
| SQ     | Sequence 2162 BP; 562 A; 565 C; 458 G; 575 T; 2 other:                    |  |      |

[illegible]

|    |      |   |      |
|----|------|---|------|
| Db | 1021 | ccaaagaaagagacaggaatcttcgaaggatccacgagatggtctggtggtggtggtg      | 1080 |
| Oy | 1107 | tgtttatcgttgcgtgcagacccattccattcacttttaccttcatttAAACCTTGGTTACAA | 1166 |
| Db | 1081 | tgctaatcgtctgctgtgacctccattccattcaatgaagcttaagccttggttaaca      | 1140 |
| Oy | 1167 | ttccagaaactacgcttccagactgtttcttggcacttgcattgctctaggtttACACAA    | 1226 |
| Db | 1141 | ttccagaactacgtcttcagagactgttcttggcactctgcatgtctctaggttaacaa     | 1200 |
| Oy | 1227 | ACAGCTGCTTCACCCAGTCTCTTTATGCATTTCTGGATGATAAACTTCAACGATGCTTCA    | 1286 |
| Db | 1201 | acaagctccaaacccagctcttctatgcatcttctgattgaataacttcaacgaatgcttca  | 1260 |
| Oy | 1287 | GAGGTTCTGTATTCCAACTCTTTCACATGAGGACAAACATCCACTGGAAATTCGTC        | 1346 |
| Db | 1261 | gagagctctgatacccaacctcttccaacaactgagagaaacacccacacgtgaatctgctc  | 1320 |
| Oy | 1347 | AGAACACTAGAGACACCCCTCCACGCGCCCAATACAGTGATGAACTAATCATCAGCTAG     | 1406 |
| Db | 1321 | agaacactagagaccacctctccacgccaataacagtgtagaaactatcatcaagctag     | 1380 |
| Oy | 1407 | AAATCTGGAGACGAATCTGCTCGTGGCCCTAACAGGGTCTCATGCCATTCGACCTT        | 1466 |
| Db | 1381 | aaatcttggaaagcagaaactgcttcgcttgccttaacagtgctcatgcatcttcgaactt   | 1440 |
| Oy | 1467 | CACACAGCTTAGAAGCCACCATGTATGTGGAGACAGCTTGCTCAAGAAATGTAGAGAG      | 1526 |
| Db | 1441 | caccaagctttagaagccaacatgatagtgaaacaggttgccttcaagaatggttagagag   | 1500 |
| Oy | 1527 | CTCTAATTTCTTAGAAGATGACCTGCTTTAGTGATCCCAACCTTTCTCTCTGGACA        | 1586 |
| Db | 1501 | ctctaatctcttagaagaagtgctactttagtgtaatccaactcttctctctcgscac      | 1560 |
| Oy | 1587 | CTCTGCTCTGCACATTAGAGG 1607                                      |      |
| Db | 1561 | ctctgctctgcacattagagg 1581                                      |      |

|          |  |
|----------|--|
| RESULT   | 4  |
| AAV61995 |  |
| ID       | AAV61995 standard; cDNA; 2162 BP.                                      |
| XX       |  |
| AC       | AAV61995;  |
| XX       |  |
| DT       | 11-JAN-1999 (first entry)  |
| DE       | Human mu-opioid receptor cDNA variant 11.                              |
| XX       |  |
| KM       | Mu-opioid receptor; variant; polymorphism; mutant; detection; disease; |
| KW       | predisposition; addiction; analgesic; anaesthetic; anti-addictive;     |
| KX       | psychopharmacological agent; diagnostic; side effect; drug; opiate;    |
| KW       | cocaine; inherited alcoholism; human; ss.                              |
| XX       |  |
| OS       | Homo sapiens.  |
| OS       | Synthetic.   |
| XX       |  |
| FH       | Key  |
| FT       | CDS  |
| FT       | Location/Qualifiers  |
| FT       | 213..2040  |
| FT       | /+tag= a   |
| FT       | /product= "mu-opioid receptor"   |
| FT       | 502..503   |
| FT       | /+tag= b   |
| FT       | /note= "Site of intron 1"  |
| FT       | 855..856   |
| FT       | /+tag= C   |
| FT       | /note= "Site of intron 2"  |
| FT       | 1376..1377   |
| FT       | /+tag= d   |
| FT       | /note= "Site of intron 3"  |
| FT       | 1613   |
| FT       | /+tag= e   |
| FT       | /note= "Wild type G is replaced by C"                                  |

XX WO9833937-A2.  
 PN 06-AUG-1998.  
 PD 02-FEB-1998; 98WO-DE00382.  
 XX 03-FEB-1997; 97DE-1003925.  
 XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
 PA Hoehe M, Wendel B;  
 PI WPI, 1998-437487/37.  
 DR  
 XX  
 XX New genomic and cDNA sequences encoding human mu-opioid receptor -  
 PT used, e.g. to predict pre-disposition to addiction and for  
 PT development of analgesics, anaesthetics and anti-addiction agents  
 XX  
 PS Claim 8; Page -: 26pp; German.  
 XX  
 XX This sequence encodes a novel human mu-opioid receptor in which a G  
 CC nucleotide at position 1613 of the wild-type sequence represented in  
 CC AAV61984 is replaced by a C. The wild type receptor and its variants,  
 CC polymorphisms and mutants are used in a method for detecting  
 CC predisposition to disease, particularly addictive disease, by isolating  
 CC DNA from a sample, genotyping selected positions and comparing with a  
 CC reference DNA. Such sequences are used to develop analgesic,  
 CC anaesthetic, anti-addictive and psychopharmaceutical agents, to construct  
 CC genes and vectors, particularly for pharmaceutical development, to  
 CC develop diagnostic kits for predicting risk of addiction, response to  
 CC analgesics or anaesthetics, or development of side effects from a drug.  
 CC Particular applications are to determine risk of addiction to opiates or  
 CC cocaine, or of developing inherited alcoholism.  
 CC Note: This sequence is not represented in the specification and has  
 CC been constructed from the wild-type sequence represented in AAV61984 in  
 CC accordance with the specification.  
 XX

| Query Match           | 97.1%          | Score 1562.6   | DB 19    | Length 2162 |
|-----------------------|----------------|--|----------|-------------|
| Best Local Similarity | 99.7%          | Pred. No. 0  |          |             |
| Matches 1576          | Conservative 0 | Mismatches 4   | Indels 1 | Gaps 1      |
| QY                    | 28             | TGGGAGGGGGCGCTATACGAGAGAGAAATGTACAGAGCTCAGCTCGCTCCCTCCGCGCTGA    | 87       |             |
| Db                    | 1              | tgggagggggcatalacgacagaggaagaaagtlcaagaagccagctcggtcccccgcgcga   | 60       |             |
| QY                    | 88             | CGCTCCTCTCTGTGTCACACCCAGAGACTGGCTTCTGTAAACACAGCAGAGAGCTGTGGAGC   | 147      |             |
| Db                    | 61             | cgtctctctctgtctccagcagagactggtttctglaagaaacagagagagctgtgagcgc    | 120      |             |
| QY                    | 148            | GGCGAAGAGAAAGCGGCTAGAGCGCTTGGACACCCGAAAAGTCTGGTGTCTGCTACT        | 207      |             |
| Db                    | 121            | ggcgaagaagagcggctgagagcgcttggaaacccgaaagatcgtgltcctgtgtacct      | 180      |             |
| QY                    | 208            | CGCACAGC - GTCGCCCGCCCGGCGCTGCACTTACCATTGAGACAGAGCGCTCCGCCAGAACG | 266      |             |
| Db                    | 181            | cgcagaagcggggtgccccgcgcgacgtlcaatlaacatgaaagcagcgctgcccccaagacg  | 240      |             |
| QY                    | 267            | CCAGCAATTGCACGTATGCCCTTGGCGTACTCAAGTTGCTCCCCAGACACCCAGCCGGTT     | 326      |             |
| Db                    | 241            | ccagaacatctgactlgtatcctctgtggtatcctaagtlgttcccccagacacagccccggtt | 300      |             |
| QY                    | 327            | CTTGGGTCGAACCTTGGCCACTTAGATGGCAACGTCCTCGACCCATGAGGGTCCGAACGCA    | 386      |             |
| Db                    | 301            | cctgtgtcaactctgtgcccaacttagatggaacactgtccgacctaatgtgtctgcaacgcga | 360      |             |
| QY                    | 387            | CCGACCTTGGGGCGGAGAGACAAGCCTGTGCCCTCCGACCCGAGAGTCCCTCATGTATCAGG   | 446      |             |
| Db                    | 361            | ccaactctggcggaggaacacagcctgttccctccgacccgagctccctccatgatacagg    | 420      |             |

QY 447 CCATCAGCATGAGCCCTTACTCATCGTGGTGGGGCTCTTGGAACTTCC 506  
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 Db 421 ccatcagcatgagcccttactcatcgltggtggtgggctcttcggaacttcc 480  
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 QY 507 TGGTCATGATGTGATGTGATGATACACCAAGATGAAGACTGCCACCAATCTACTTT 566  
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 Db 481 tggtcatagtatgtatgtatgatacacaagaatgaagactgcccacacatcactt 540  
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 QY 567 TCAACTTGTCTGGAGATGCTTACGCCACAGTACCTGCCCTTCAGAGTGTGAAT 626  
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 Db 541 tcaacttgtctggagatgctttagccacagtaacctgccttcacagtgtaatt 600  
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 QY 627 ACCTAATGGAGACATGGCCATTTGGAACCATCTTTGCAAGATAGTATCCATAGATT 686  
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 Db 601 acctaatggagacatggccatttggaaacatcttggcaagatagatctccatagatt 660  
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 QY 687 ACTATACATGTTACACAGATATTCACCTCTGACACATGAGGTGTGATGATCTTG 746  
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 Db 661 actatacatgttccacagatatccctctgcacacatgagtgtatcgaatctg 720  
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 QY 747 CAGTCTGCCACCTGTCAAGGCTTATAGATTCCGTACTCCCGCAATGCCAAATTTATCA 806  
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 Db 721 cagtcgcacctgtcaagaccttagattccgtactcccgaaatgccaataatca 780  
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 QY 807 ATGTCTGCAACTGAGATCTCTTTCAGCCATTTGGTCTTCTGTAATGTTGATGGCTACAA 866  
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 Db 781 atgtctgaactgatctctcttccagcaattgtcttctgtaatgtlcatagctacaa 840  
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 QY 867 CAAATATACAGCAAGTTCATAGATGTGATGATTAATCTCTCATCCAACTGGTACT 926  
 |||||||  
 Db 841 caaatatcagcaaggttcatagatgtacactaaatctctcaccacactggaact 900  
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 QY 927 GGGAAAACTGCTGAAGATGTGTTTTCATCTTCCGCTTCATATGSCAGTGTCTATCA 986  
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 Db 901 gggaaaaactgctgaagatgtgttttcatcttccgcttcatatagccagtgctacaa 960  
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 QY 987 TTAACGTGTCTATGACATGATGATCTTGGCCTCAAGAGTGTCCGATCTCTTGCT 1046  
 |||||||  
 Db 961 ttacgtgtgtctatgactgatctgtgcctcaagagtgccagatgctctctgct 1020  
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 QY 1047 CCAAGAAAAAGGAGAGATCTTCAAGATCAACGAGATGAGTGTGGTGGTGGCTG 1106  
 |||||||  
 Db 1021 ccaagaaaaaggaagaaatcttcgaagatccacgaagatgagtggtggtgctg 1080  
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 QY 1107 TGTTCATGCTGTCTGACTCCCATTCACATTTACGTATCAATTAAGCCTTGTTACAA 1166  
 |||||||  
 Db 1081 tgttcactgtctgtgactcccatccaatcttaagcatcatatgaagccttggttacaa 1140  
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 QY 1167 TCCAGAACTACGTTTCAGACTGTTTCTTGGACATTTGCTGCTAGTTTACAA 1226  
 |||||||  
 Db 1141 tccagaaactacgttccagactgttcttgcacttctgcatctgcttagtlaacaa 1200  
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 QY 1227 ACAGCTGCCCTCAACCCAGTCTTATGCAATTTGATGTAAGAACTTCAACGATGTCTCA 1286  
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 Db 1261 gagagttctgtatcccaactcttccaacttgaagacaaaactccactcgatctgctc 1320  
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 Db 1381 aaatatctggaagcaaaactgctccgttgccttaaaaggttccatgccaatccgactt 1440  
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 QY 1467 CACCAAGCTTAGAAGCACCATGATGTGAGACAGATTCTTCAAGAAATGTGAGAG 1526  
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 Db 1441 caccaagcttagaagcaccaatgtatgtggaagcaggttctccaagaatgttgaagag 1500  
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 QY 1527 CTCTAATCTCTAGGAAAGTGCTGCTTTAGTGCATCCAACTCTTCTCTCTGAGCA 1586  
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Db 1501 cctcaatctctaggaagagctactttagtgcataccaactcttccctctgcca 1560  
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 Db 1561 cctctgctctgcacattagaag 1581  
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RESULT 5  
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 ID AAV61985 standard; cDNA: 2162 BP.  
 XX  
 AC AAV61985;  
 XX  
 DT 11-JAN-1999 (first entry)  
 XX  
 DE Human mu-opioid receptor cDNA variant 1.  
 XX  
 KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;  
 KW prediagnosis; addiction; analgesic; anaesthetic; anti-addictive;  
 KW psychopharmacological agent; diagnostic; side effect; drug; opiate;  
 KW cocaine; inherited alcoholism; human; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT CDS 213..2040  
 FT /tag= a  
 FT /product= "mu-opioid receptor"  
 FT misc\_feature 502..503  
 FT /tag= b  
 FT /note= "Site of intron 1"  
 FT 855..856  
 FT /tag= c  
 FT /note= "Site of intron 2"  
 FT misc\_feature 1376..1377  
 FT /tag= d  
 FT /note= "Site of intron 3"  
 FT 41  
 FT mutation  
 FT /tag= e  
 FT /note= "Wild type G is replaced by T"  
 FT  
 PN WO9833937-A2.  
 XX  
 PD 06-AUG-1998.  
 XX  
 PF 02-FEB-1998; 98WO-DE00382.  
 XX  
 PR 03-FEB-1997; 97DE-1003925.  
 XX  
 PA (DELB-) DELBRUCK CENT MOLEKULARE MEDIZIN MAX.  
 XX  
 PI Hoehe M, Wende B;  
 PT  
 DR  
 XX  
 WP1: 1998-437487/37.  
 XX  
 PT New genomic and cDNA sequences encoding human mu-opioid receptor -  
 used, e.g. to predict pre-disposition to addiction and for  
 development of analgesics, anaesthetics and anti-addiction agents  
 PT  
 XX  
 PS Claim 8: Page -: 26p; German.  
 XX  
 CC This sequence encodes a novel human mu-opioid receptor in which a G  
 CC nucleotide at position 41 of the wild type sequence represented in  
 CC AAV61984 is replaced by a T. The wild type receptor and its variants,  
 CC polymorphisms and mutants are used in a method for detecting  
 CC prediagnosis to disease, particularly addictive disease, by isolating  
 CC DNA from a sample, genotyping selected positions and comparing with a  
 CC reference DNA. Such sequences are used to develop analgesic,  
 CC anaesthetic, anti-addictive and psychopharmacological agents, to construct  
 CC genes and vectors, particularly for pharmaceutical development, to  
 CC develop diagnostic kits for predicting risk of addiction, response to

50 Sequence 2162 BP; 562 A; 565 C; 457 G; 576 T; 2 other;

Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

[illegible]

|    |      |  |      |
|----|------|--|------|
| OY | 927  | GGGAAACCTGCTGAACATGTCGTGTTTCAATGTCGCTTCATTTATGCAAGTGCATCA      | 986  |
| Db | 901  | gggaaaacctcgagaaatctcglttcaatcttcgcttccatctatgccaagtctcaca     | 960  |
| OY | 987  | TTACCGTGTGCTATGAGCTGATGATCTTGCGCCTCAAGAGTGTCCGATGCTCTGTGGCT    | 1046 |
| Db | 961  | ttaccgtgtgtatgagactgatctgtgcctcaagagtctccgaatgctctctgct        | 1020 |
| OY | 1047 | CCAAGAAAAAGNAGGAATCTTGGAAGATCACCGAATGSGTGGTGGTGGGCGTG          | 1106 |
| Db | 1021 | ccaaagaaagaaagaaatcttcgaagatcaaccaagatgctcgtgagtgagtg          | 1080 |
| OY | 1107 | TGTTTACATGCTGTGCTGGACACCCATTCCACATTATGCTCATATTAACCTTGGTTACAA   | 1166 |
| Db | 1081 | tgttatcgtctgtgtgagacccattccacattagctcatatgaagccttggtacaa       | 1140 |
| OY | 1167 | TCCCAAGAACTAGCTTCCCAACAGTCTTTTGGACTTTCGACTTTCCTTAGTATACAA      | 1226 |
| Db | 1141 | tcccaagaactagcttcccaacagcttcttgcacttcgcatgctctagttacaa         | 1200 |
| OY | 1227 | ACAGCTGCCTCAACCCAGTCTTTATGCAATTTCTGGATGAATAACTTCAAGAGTCTTCA    | 1286 |
| Db | 1201 | acagctgcctcaaccagctcctttagcatctctgataigaaacttcaaaogatgcttca    | 1260 |
| OY | 1287 | GAGAGTTCTGTATCCCAACTCTTCCAACTTGAGCACAACAAACTCCACTGGAATTGTC     | 1346 |
| Db | 1261 | gagagttctgtatcccaactcttccaacatbagaagaanaactccactcgaattctc      | 1320 |
| OY | 1347 | AGAACCTAGAGACACACCCCTCCACGGCCCAATTCAGATGATGAAGACTTATCATCAGCTAG | 1406 |
| Db | 1321 | agaaactatagagaccacctccaagccaatacagtgatagaactaatacaccagctag     | 1380 |
| OY | 1407 | AAAACTGGAAGCAGAAACTGTCGCTGTGCGCTTAACAGGGTCTCATGCCATTCCGACCTT   | 1466 |
| Db | 1381 | aaaactcgtgaagcagaaactgctcgttgccttaacaagtgctcatgcatccgaactt     | 1440 |
| OY | 1467 | CACACACTTAGAAGCCACCATGATGTGGAGACAGCTTGCTTCAAGATGATGAGAGG       | 1526 |
| Db | 1441 | caccaagcttagaagccaacatgatagtggaacagatgttgcctcaagaatgtagtaggg   | 1500 |
| OY | 1527 | CTCTAAATTTCTTAGAAGAGTCCCTGCTTTTAGTGTCATCCAACTCTTTCCTCTGGACA    | 1586 |
| Db | 1501 | ctctaaattctctagaaagtgcctactctttagtcatccaacctcttccctctctcgaca   | 1560 |
| OY | 1587 | CTCTGCTCTGCACATTAGAGG 1607                                     |      |
| Db | 1561 | ctctgctctgacaattagagg 1581                                     |      |

|          | RESULT   | 6                              |
|----------|--|--------------------------------|
| AAV61986 | AAV61986   |                                |
| ID       | AAV61986   | standard; cDNA; 2162 BP.       |
| XX       |  |                                |
| AC       | AAV61986;  |                                |
| XX       |  |                                |
| DT       | 11-JAN-1999  | (first entry)                  |
| XX       |  |                                |
| DE       | Human mu-opioid receptor cDNA variant 2.                               |                                |
| XX       |  |                                |
| KW       | Mu-opioid receptor; variant; polymorphism; mutant; detection; disease; |                                |
| KW       | predisposition; addiction; analgesic; anesthetic; anti-addictive;      |                                |
| KW       | psychopharmaceutical agent; diagnostic; side effect; drug; opiate;     |                                |
| KW       | cocaine; inherited alcoholism; human; ss.                              |                                |
| XX       |  |                                |
| OS       | Homo sapiens.  |                                |
| OS       | Synthetic.   |                                |
| XX       |  |                                |
| FT       | Key  | Location/Qualifiers            |
| FT       | CDS  | 213..2040                      |
| FT       |  | /*tag= a                       |
| FT       |  | /product= "mu-opioid receptor" |
| FT       | misc_feature   | 502..503                       |



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FT FT /tag= b /note= "Site of intron 1"
FT FT /note= "855..856"
FT FT misc_feature /tag= c
FT FT /note= "Site of intron 2"
FT FT misc_feature 1376..1377 /tag= d
FT FT /note= "Site of intron 3"
FT FT mutation 80
FT FT /tag= e
FT FT /note= "Wild type C is replaced by T"
XX XX
XX PN WO9833937-A2.
XX PD
XX PD 06-AUG-1998.
XX XX
XX XX 02-FEB-1998; 98WO-DE00382.
XX XX
XX PR 03-FEB-1997; 97DE-1003925.
XX XX
XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX PI Hoehe M, Wendel B;
XX XX
PS WPI: 1998-437487/37.
CC CC This sequence encodes a novel human mu-opioid receptor in which a C
CC nucleotide at position 80 of the wild-type sequence represented in
CC AAV61984 is replaced by a T. The wild type receptor and its variants,
CC polymorphisms and mutants are used in a method for detecting
CC predisposition to disease, particularly addictive disease, by isolating
CC DNA from a sample, genotyping selected positions and comparing with a
CC reference DNA. Such sequences are used to develop analgesic,
CC anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
CC genes and vectors, particularly for pharmaceutical development, to
CC develop diagnostic kits for predicting risk of addiction, response to
CC analgesics or anesthetics, or development of side effects from a drug.
CC Particular applications are to determine risk of addiction to opiates or
CC cocaine, or of developing inherited alcoholism.
CC Note: This sequence is not represented in the specification and has
CC been constructed from the wild-type sequence represented in AAV61984 in
CC accordance with the specification.
CC xx
CC xx
SO Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other;

Query Match 97.0%; Score 1561; DB 19; Length 2162;
Best Local Similarity 99.6%; Pred No. 0;
Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1

OY 28 TGGGAGGGGGCTATACGCAGAGAGAATGTCAAGATCCTAGCTCGTCCCTCCGCTGA 87
Db 1 tgggagggggcctatacgacagagagaatgtcaagtctcagctcgctccctcgactga 60
OY 88 CGCTCTCTCTGTCTTCACGCCAGACTGGTTTCTGTAAAGAACAGCAGAGCTGTGGCAGC 147
Db 61 cgctctctcttcttcacagtaagtaagtggtttcttgtlaagaacaagcagagagcttgcagc 120
OY 148 GGCGAAGCAACGGCGTGAGGGCGCTTGGAAACCGAAAAGTCGCGGTGCTCCGGTACCT 207
Db 121 ggcgaaggaaagcggcgtgcagcgttggaaaccggaaaagtlctcgtgcgtcctgcacct 180
OY 208 GCACACAGC-GTGTCCCGCGCGCGCGCTGACATGACAGACAGACGCTGCCCCACGAACG 266
Db 181 gcgaacagcgtgtcccgcgccgcgcgtcacatgaacagcagcgtgcgtcccccaagaag 240
OY 267 CCAGCAATTGCATGATGCCCTTGGCGTACGAATTGTCGCCAGCACCCAGCCCAGGTT 326

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|    |      |                        |  |                |      |
|----|------|------------------------|--|----------------|------|
| Db | 241  | ccagaacattgcacgcga     | cgccctggcgtgctgctacccaagttcgcctcccaagca          | cccccggtt      | 300  |
| OY | 327  | CTGTGGTCAACCTTTGCCACTT | AGATGGCAACCTGTCCGACCCCATGCGGGTCCGAACCGCA         | 386            |      |
| Db | 301  | ccctgggtcaactctgtcc    | acttagatgagcaacctctgcgaaccctctcgaccocatg         | cgtctcgaaacgca | 360  |
| OY | 387  | CCGACCTGGCGCGGAGAGAC   | AGCCTGTGGCCTTCGACCGGCAKGTCCCTTCATGATCAGG         | 446            |      |
| Db | 361  | ccaacttggcgaggagaa     | gacgcctctgtcccttcgacgcgcgactccctccatgatac        | gacg           | 420  |
| OY | 447  | CCATACGATCATG          | GCCCTCACMCCATCGTGTGGGTGGGGGCTTCGGAAATCC          | 506            |      |
| Db | 421  | ccatcaacgatac          | gagccctctacccaatcg                               | tg             | 480  |
| OY | 507  | TGTGTATATGATGATTTGT    | CAGATACACCAAGATGGAAGTCACTCCACCAATCATCATTT        | 566            |      |
| Db | 481  | tggtcatatgata          | gtatgtgtcaagatacccaagatgaaagctgcacacaacatcata    | ctt            | 540  |
| OY | 567  | TCAACCTTGCTGTGGCAG     | ATGCTTTAGCCACGATACCTGCCCTTCAGAGTGTGAAT           | 626            |      |
| Db | 541  | lcaacctgtccttgcg       | agatgaccttagccaccagtaaccctgcacctccagag           | tg             | 600  |
| OY | 627  | ACCTAATGGGAACAT        | TGGCCATTTTGGAAACCATCCTTTGCAAGATAGTATCTCCATAGAT   | 686            |      |
| Db | 601  | acctaaatgggaaca        | tgagccatttggaaacccctcttgcgaagatgagatctcata       | gatt           | 660  |
| OY | 687  | ACTAATACATTTTAC        | CAGATATTTACCCCTGCAACATGATGTTGATCATGAT            | 746            |      |
| Db | 661  | actatacaatg            | ttaaccagatatataccctctgcacacatgagtg               | tgtatgatacattg | 720  |
| OY | 747  | CAGTCTGCCACCTGTCA      | AGGCTTTAGATTTCCGTACTCCCGAAATGCCAAATTAAT          | 806            |      |
| Db | 721  | cgatctgcaccctgtca      | agagcccttagattctcgatactccggaaatgcaaaaattaca      | 780            |      |
| OY | 807  | ATGTCTGCAAT            | TGGATCTCTTTCAAGCCATTTGGTCTTCTGTAAATGTTCA         | TGGCTTAACA     | 866  |
| Db | 781  | atgtctgaaacttga        | tccctctcttcagcaattgctctccctgtaattgtcata          | tggtcataaa     | 840  |
| OY | 867  | CAAAATACAGCA           | AGGTTTCCATAGATTTGTACATTAATTTCTCATCCAACTGGT       | ACT            | 926  |
| Db | 841  | caaaatacagagca         | aggttccatagatltgtcaactaacaatctctcatccaacctgtact  |                | 900  |
| OY | 927  | GGGAAAACCTGCTG         | AAGATCTGTGTTTTCACTTTCGCCCTTCAATTATGCCAGTGC       | ATCA           | 986  |
| Db | 901  | gggaaaacctgcga         | atgactgtgtttcatactctgccttcaatbatgcag             | ggtctcata      | 960  |
| OY | 987  | TTACCGTGTGT            | ATGAGCTATGATCTTGGGCTCAAGAAGTTCGGCATGCTCTTGCT     |                | 1046 |
| Db | 961  | ttaccgtgtgtgata        | tgagactgtatctcttgccctcaagaagtgctcgatgcctctgtgct  |                | 1020 |
| OY | 1047 | CCAAAGAAAAGAGAC        | GAATCTTCGAAGATCCAGATGTTGCTGGTGGTGGTGGTGG         | CGTG           | 1106 |
| Db | 1021 | ccaaagaaaaggaaga       | gaatccttcgaaagataccagatggtgtgtgtgtgtgtgtgtgt     |                | 1080 |
| OY | 1107 | TGTTATCGTCTGCTG        | AGCTCCATTTCACATTTTACGTCAATTAAGCTTGTGTTACA        |                | 1166 |
| Db | 1081 | tgttatcgtctgtgtga      | atccatccaattagctcaatlaaagcctgtgttaca             |                | 1140 |
| OY | 1167 | TCCCAAGAACTAC          | GTTCACAAGCTTTTCTTGGACCTTTCGATTTGCTGTAGTTAT       | CACAA          | 1226 |
| Db | 1141 | tcccaagaatac           | gtgttccagactgttctctgtgacactctgcatagtctctaggttata | caaa           | 1200 |
| OY | 1227 | ACAGTGGCTCAAC          | CCCGTCTTTATGATTTTGGATTAATAACTTCAACAGATGCTTCA     |                | 1286 |
| Db | 1201 | acagctgcctcaac         | cccgctcttatagtcatcttcgatagtgaaaaacttcaaa         | gagatcttca     | 1260 |
| OY | 1287 | GAGAGTTCTGTAT          | CCCAACCTTTTCCAACTTGTAGCAACAAACATTCAC             | TGGAATTCGT     | 1346 |
| Db | 1261 | gagagttctgtata         | tcccaacctcttccaacttgagaaacaaactccac              | ctcgtgaattgtc  | 1320 |
| OY | 1347 | AGAACTAGAGAC           | CACTCCATCGGCCCAATACAGTGAATGAAC                   | TAACTATCAGCTAG | 1406 |

Db 1321 agaacactagagagaccacctccagcgccaatacagtagatagaactaatcatcagctag 1380  
 QY 1407 AAAATCTGAGAGAGAACTGCTCCGTCGCCCTAACAGAGGATTCATCCATTCGACCTT 1466  
 Db 1381 aaatctgagagagaaactgctcgccttgccctaaacagggtctcagcatccgcagcctt 1440  
 QY 1467 CACCAAGCTTAGAGGCCACCATGTATGTGAGAACAGAGCTTTCAGAAATGTGTAGAGG 1526  
 Db 1441 caccagactagagagcaccatgtagtgaagcaggtctgctcaagaatgtagtagag 1500  
 QY 1527 CTCTATTCTCTAGAGAAAGGCTGCTTTAGGTATCCAACTCTTCTCTGAGCA 1586  
 Db 1501 ctctaatctcctagagaaatgctcactcttagagtagcaccactctcctcctgagca 1560  
 QY 1587 CTCTGCTCTGACATTAGAGG 1607  
 Db 1561 ctctgctctgacattagag 1581

RESULT 7  
 AAV61987  
 ID AAV61987 standard: cDNA: 2162 BP.  
 AC AAV61987:  
 XX  
 DT 11-JAN-1999 (first entry)  
 XX  
 DE Human mu-opioid receptor cDNA variant 3.  
 XX  
 KM Mu-opioid receptor; variant; polymorphism; mutant; detection: disease;  
 KW predisposition; addiction; analgesic; anesthetic; anti-addictive;  
 KW psychopharmacological agent; diagnostic; side effect; drug; opiate;  
 KW cocaine; inherited alcoholism; human; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT CDS 213..2040  
 FT /tag= a  
 FT /product= "mu-opioid receptor"  
 FT misc\_feature 502..503  
 FT /tag= b  
 FT /note= "Site of intron 1"  
 FT misc\_feature 855..856  
 FT /tag= c  
 FT /note= "Site of intron 2"  
 FT misc\_feature 1376..1377  
 FT /tag= d  
 FT /note= "Site of intron 3"  
 FT mutation 102  
 FT /tag= e  
 FT /note= "Wild type C is replaced by T"  
 XX  
 PN WO9833937-A2.  
 PN  
 PD 06-AUG-1998.  
 XX  
 PF 02-FEB-1998: 98WO-DE00382.  
 PR 03-FEB-1997: 97DE-1003925.  
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
 XX  
 PI Hoehe M, Wendel B;  
 XX  
 DR WPI, 1998-437487/37.  
 PT New genomic and cDNA sequences encoding human mu-opioid receptor -  
 PT development, e.g. to predict pre-disposition to addiction and for  
 PT development of analgesics, anaesthetics and anti-addiction agents  
 XX  
 PS Claim 8: Page -: 26pp: German.

XX This sequence encodes a novel human mu-opioid receptor in which a C  
 CC nucleotide at position 102 of the wild-type sequence represented in  
 CC AAV61984 is replaced by a T. The wild type receptor and its variants,  
 CC polymorphisms and mutants are used in a method for detecting  
 CC predisposition to disease, particularly addictive disease, by isolating  
 CC DNA from a sample, genotyping selected positions and comparing with a  
 CC reference DNA. Such sequences are used to develop analgesic,  
 CC anesthetic, anti-addictive and psychopharmacological agents, to construct  
 CC genes and vectors, particularly for pharmaceutical development, to  
 CC develop diagnostic kits for predicting risk of addiction, response to  
 CC analgesics or anaesthetics, or development of side effects from a drug.  
 CC Particular applications are to determine risk of addiction to opiates or  
 CC cocaine, or of developing inherited alcoholism.  
 CC Note: This sequence is not represented in the specification and has  
 CC been constructed from the wild-type sequence represented in AAV61984 in  
 CC accordance with the specification.  
 XX  
 SQ Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other:

Query Match 97.0%; Score 1561; DB 19; Length 2162;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
 QY 28 TGGAGAGGGGCTATACGAGAGAGATGTCAGATGCTCAGCTCCCTCCGCTGGA 87  
 Db 1 tggagaggggcatatagcagagagatgtagatgctcagctcgtccctccgcctga 60  
 QY 88 CGCTCTCTCTGCTCTGACGAGCAGCTGTTTCTGTAAAGAAAGAGAGAGCTGTGACAC 147  
 Db 61 cgtctctctctgctctgacgagacgctgttctgttaagaaatagagagagcgtgtgacg 120  
 QY 148 GGGGAAAGAGAGGGGCTGAGGCGCTTGAACCGGAAATCTCGGCTCTGCTGACCT 207  
 Db 121 ggcgaagagagagagagctgagcgcttgagaaacggaaagctcgtgtgctccgtacct 180  
 QY 208 CGCAGAGC-GTGGCCGCCCGCGGCTGACGATGACAGAGAGAGCGTGGCCCGCAGAGC 266  
 Db 181 cgcagagcggtgcccgcgcgcgcgtacatgacagagcagcgctgcccacagagc 240  
 QY 267 CCAGCAATTGACATGATGCTTGGGCTACTCAAGTTGCTCCCGACAGCAGCCCGGTT 326  
 Db 241 ccagcaattgactgactgcttggcgtactcaagtgtctcccaagaccacgcccgggt 300  
 QY 327 CCGGGTCAACTGTGCCACTTAGATGCAACCTGTCCAGCCATGCGGTCCGAACCGCA 386  
 Db 301 ccgggtcaactgtgccacttagatgcaacctgtccgaaccatgagcgtccgaacgca 360  
 QY 387 CCGACCTGGGCGGAGAGAGAGAGCTGTGCTCCGACCGAGTCCCTCCATGATCACGG 446  
 Db 361 ccaacttgccggagagagcagcctgtgcccgcagcagcgagctccctcatgatacgg 420  
 QY 447 CCATCAGCATGATGCGCCCTCTACTCCATGCTGTGGTGGGCTCTTGGAAACTTCC 506  
 Db 421 ccatcagcatgagccctctactccatcggtgtggtggtgtgtcgttcggaactcc 480  
 QY 507 TGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566  
 Db 481 tggtcattgattgattgattgattgattgattgattgattgattgattgattgattgatt 540  
 QY 567 TCAACCTTCTCTGAGATGCTTAGCCACCATGATGATGATGATGATGATGATGATGAT 626  
 Db 541 tcaacttctctgagatgcttagccacagatgattgattgattgattgattgattgatt 600  
 QY 627 ACCTAATGGGAATGAGCATTTGGAACCATGCTTTGCAAGATGATGATGATGATGAT 686  
 Db 601 accataatgggaatgagcatgttgaaacatcttggacaagatgattgattgattgatt 660  
 QY 687 ACTATTAATGTTTCCACCATATTCACCTCTGACCAATGATGATGATGATGATGATGAT 746  
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QY 747 CAGTCTCCACCCCTGTCAGAGCCCTTAGATTTCCGTACTCCCGGAATGCCAAATATATCA 806
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QY 807 ATGCTGCAACTGGATCTCTCTTACCCATTGGTCTTCTGTAATGTTACATGGCTACAA 866
    |||||||
Db 781 atgtctgcaactggatctctcttcaagcatttgcttcctgtaatttcatgctacaa 840
QY 867 CAAATATCAGGCAAGGTTCCATAGATGTAACATTAATCTCTCATCCCAACCGGTACT 926
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QY 927 GGGAAACCTGCTGAAGATCTGTGTTTTCATCTTCCGCTTCAATATGCGATGCTCATCA 986
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Db 901 gggaaacctcgtgaagatctgtttctatcttcgcttcatatgccaagtcgactca 960
QY 987 TTACCGTGTGCTATGACTGATGATCTTGGCCCTCAAGAGTGTCCGATGCTCTGGCT 1046
    |||||||
Db 961 ttaccgtgtctatgactgactgactctgacctcaagaagtgctcgcactgctctgct 1020
QY 1047 CCAAGAAAAGGACAGGATCTTGAAGGATCACAGAGTGCTGTGGTGGTGGCTG 1106
    |||||||
Db 1021 ccaagaaagagcaggaatctctcgaagatcaccaagagatggtgctggtgctg 1080
QY 1107 TGTTCATGCTCTGCTGAGCTCCCATTCACATTTACGTCATCATTAAGCCCTTGGTTCAA 1166
    |||||||
Db 1081 tgttcactgctctgtagctcccatcattacattacgctcattaaagccttggttcaaa 1140
QY 1167 TCCCAAGAACTAGCTTCCACACATGTTTGGCACTTCTGATTTGCTGTAGTTACCAA 1226
    |||||||
Db 1141 tcccaagaactagcttcccaagactgtcttgacactctgcatgctctgagttaccaa 1200
QY 1227 ACAGCTGCTCAACCCAGTCTTATGATTTTGATGTAAGAACTTCAACGATGCTTCA 1286
    |||||||
Db 1201 acagctgctccaaccccgctcttattgacttctcgatgtaaaacttaacgacttca 1260
QY 1287 GAGAGTTCTGTATCCCACTCTTCAACATTTAGACAAACAACTCCATCGAATTCGTC 1346
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Db 1261 gaaagttctgtatcccaactcttccacaacttgagcaaaaaactccacatcgaaatctgctc 1320
QY 1347 AGAAGACTAGAGCCACCCCTCCAGGCGCAATGAGTGATGAACATTAATCATCAGCTAG 1406
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Db 1321 agaagactaagagcaccctcccgccagcaatacagtgatagaaacttaactaactagctag 1380
QY 1407 AAATCTGGAAGCAAGAACTGCTCCGTTGCCCTAACAGGCTCTCATGCCATTCGACCTT 1466
    |||||||
Db 1381 aaatctggaagcagaagaactgctccgttgccctaaaggttcatgacttccgactt 1440
QY 1467 CACCAAGCTTAGAAGCCACCATGTATGTGAAGCAGGTTGCTTCAGCAATGTGAGAGG 1526
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Db 1441 caccaaagcttagaagcaccatgtatgtgaaagcaggttcttcaagaagatgtgtaagag 1500
QY 1527 CTCTAATCTCTAGGAAGGCTGCTTAAAGTCATCCAAACCTTCTCTCTGCGCCA 1586
    |||||||
Db 1501 ctctaattctctaggaagtgaccttaagtcacccaactcttctctctgcca 1560
QY 1587 CTCTGCTCTGACATTAGAGG 1607
    |||||||
Db 1561 ctctgctctgacattagag 1581

```

RESULT 8

AAV61988

XX AAV61988 standard; cDNA; 2162 BP.

XX AAV61988;

DT 11-JAN-1999 (first entry)

DE Human mu-opioid receptor cDNA variant 4.

KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease; predisposition; addiction; analgesic; anaesthetic; anti-addictive;

```

KW psychopharmaceutical agent; diagnostic; side effect; drug; opiate;
KM cocaine; inherited alcoholism; human; ss.
XX Synthetic.
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 213..2040
FT     /tag= a
FT     /product= "mu-opioid receptor"
FT     /tag= b
FT     /tag= "Site of intron 1"
FT     /note= "855..856"
FT     /tag= c
FT     /note= "Site of intron 2"
FT     /tag= d
FT     /note= "1376..1377"
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FT     /note= "Site of intron 3"
FT     /tag= e
FT     /note= "Wild type C is replaced by A"
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FT     /note= "Wild type C is replaced by A"
PN WC9833937-A2.
PD 06-AUG-1998.
PF 02-FEB-1998; 98WD-DE00382.
PR 03-FEB-1997; 97DE-1003925.
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PI Hoehe M. Mendel B:
PI WPI; 1998-437487/37.
XX New genomic and cDNA sequences encoding human mu-opioid receptor -
XX used, e.g. to predict pre-disposition to addiction and for
XX development of analgesics, anaesthetics and anti-addiction agents
XX Claim 8; Page -: 26pp; German.
PS
XX This sequence encodes a novel human mu-opioid receptor in which a C
XX nucleotide at position 175 of the wild-type sequence represented in
XX AAV61984 is replaced by an A. The wild-type receptor and its variants,
XX polymorphisms and mutants are used in a method for detecting
XX predisposition to disease, particularly additive disease, by isolating
XX DNA from a sample, genotyping selected positions and comparing with a
XX reference DNA. Such sequences are used to develop analgesic,
XX anaesthetic, anti-addictive and psychopharmaceutical agents, to construct
XX genes and vectors, particularly for pharmaceutical development, to
XX develop diagnostic kits for predicting risk of addiction, response to
XX analgesics or anaesthetics, or development of side effects from a drug.
XX Particular applications are to determine risk of addiction to opiates or
XX cocaine, or of developing inherited alcoholism.
XX Note: This sequence is not represented in the specification and has
XX been constructed from the wild-type sequence represented in AAV61984 in
XX accordance with the specification.
SQ Sequence 2162 BP; 563 A; 564 C; 458 G; 575 T; 2 other:

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Query Match 97.0%; Score 1561; DB 19; Length 2162;

Best Local Similarity 99.6%; Pred. No. 0; Mismatches 5; Indels 1; Gaps 1;

Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 28 TGGAGAGGGGCTTACGACAGAGAGATGTACATGCTGCTGCTCCCTCCGCTGA 87

Db 1 tggagagggtatagcagagagatgtacatgctgctgctccctccgctga 60

QY 88 CGTCTCTCTGCTGACGACGAGCTGTTTCTGTAAGAAACGAGGAGCTGTGACAC 147

D 61 cgcctcctctctgtctcagccagagctggttctgtlaagaaacagcagagctgtgagc 120  
Q 148 GGGGAAAGAGAGGGGCTGAGGCGCTTGGAAACCGGAAAGTCTGCTGCTGGTAACT 207  
D 121 ggggaaagagagagcgtcgtgagcgtcttggaacccgaaaagctcgtgctctgtgatact 180  
Q 208 CGCAGACG-CTGCCCGCCGCGCGCTCAGTACATGAGACAGACGCTGCCCGCAGAACG 266  
D 181 cgcacagcagctgcccgcgcgcgcagctacgtacgtacgtacgtacgtacgtacgtacgt 240  
Q 267 CCGCAATTCGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 326  
D 241 cccgacatctgacatctgctctgctgctacccaagctgctccacagaccacgcccgtt 300  
Q 327 CCGGGGTCACCTGCTCCACTTGTAGATGAGCAACCTGTCGACCCATCGGCTCGAACGCA 386  
D 301 cccgggtcaccctgtctccacttagatgagcaacctgtccgacccatcggtctcgaaaccgca 360  
Q 387 CGCAGCTGGGCGGAGAGACAGCCTGTGCCCTCCGACCGGACGCTCCCTCATGATCAGG 446  
D 361 ccaacctggcgggagagagacagcctgtgccctcgcagccgacgtccctcatgatacag 420  
Q 447 CCATCAGATCATGGCCCTTACTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 506  
D 421 ccatcagatcatgagcccttactccatcgctgctgctgctgctgctgctgctgctgctgctgct 480  
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D 481 tggctcatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat 540  
Q 567 TCAACCTGCTGTGAGATGCTTACGACACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 626  
D 541 tcaacctgtctgtgagatgcttgcacacagctacccctgccttcagagctgctgctgctgctgct 600  
Q 627 ACCGAATGGGAATGGGCACTTGGAAACCTGCTTGGAAAGATGATGATGATGATGATGATGAT 686  
D 601 acctgaatgggaatgggcaacttggaaacacttcttgcagaaagatgctgctgctgctgctgctgct 660  
Q 687 ACTATAACATGTTACACGATATACCTGCTGACACGATGATGATGATGATGATGATGATGAT 746  
D 661 actataacatgttacacgatatatcaacctctgcacacagagtgctgctgctgctgctgctgctgct 720  
Q 747 CAGCTGCGACCTGTCAAGGCTTATGATTTCCGTACTCCCGGAAATGCCAAATATTATCA 806  
D 721 cagctgcgacacctgtcaaggtcttagattctcgtactcccgaaatgccaaatattatca 780  
Q 807 ATGCTGCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 866  
D 781 atgctgcgaaatgatactctctctcagccatgtgcttctcgtactgctgctgctgctgctgctgct 840  
Q 867 CAAATATACAGGCAAGGTTCCATGATTTGTACATTAACATTTCTCATCCAACTGGTACT 926  
D 841 caaatatcacaggcaaggttccatgatatgtacataaactctctcatccaaactgtgctgctgctgct 900  
Q 927 GGGGAAACCTGTGAAGATCTGTGTTTTCATCTTCCGCTTCAATTATGCGAGTCTCATCA 986  
D 901 ggggaaacctgtgaagatctgtgttctcattctgctgctgctgctgctgctgctgctgctgctgct 960  
Q 987 TTTACCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1046  
D 961 ttacccgtgtgctatgagctgagatcttgcctcctcagaaatgtcgcgatagtctctgctgctgct 1020  
Q 1047 CCAAGAGAGAGAGAGATTTTGAAGATCACAGAGATGATGATGATGATGATGATGATGATGATGAT 1106  
D 1021 ccaagagagagagagagatcttgcgaaatgtcgcgaaatgtcgcgaaatgtcgcgaaatgtcgcgaa 1080  
Q 1107 TGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1166  
D 1081 tgttcacgtctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1140  
Q 1167 TCCGAGAACTAGTTCACAGATGTTCTTGGAGATTTGCTGATGCTGATGCTGATGCTGATGCTGAT 1226  
D 1141 tcccagaaactagcttccagacgttctctgagcacttgcgacttgcgacttgcgacttgcgacttgcgact 1200

Q 1227 ACAGCTGCCCTCAACCCAGTCCCTTTATGATTTCTGATGATAAACTTCAACGATGCTTCA 1286  
D 1201 acagctgctcacaacccagctccttctgacttctgtagtgaataactcacaagatgcttca 1260  
Q 1287 GAGAGTTGTGTATCCCAACCTCTTCCAACTTGTAGAGCAACAAACTCTCACTCGAATTCGTC 1346  
D 1261 gagagttgtgtatcccaactcttccaaacttgaagaaataactcgaatcgtc 1320  
Q 1347 AGAAGACTAGAGACACCCCTCCAGGCGCAATPACATGATGAACTAATCAATCACTGATG 1406  
D 1321 agaagactagagacacccctccagcgccaatacagtgatgataactcaacagctag 1380  
Q 1407 AAAATCTGGAAGCAGAAACCTGCTCCCTTGCCTTAACAGGCTTCATGCCATTCGACCTT 1466  
D 1381 aaatctggaagcagaactcgtcgtctgctccctaaaggtctcatcgtccatccgacct 1440  
Q 1467 CACCAAGCTTTAGAGCCACCATGTATGTGGAAGCAGGTTGCTTCAAGATTTGTAGAGAG 1526  
D 1441 caccaagcttgaagccacatgtatgtgaagcaggttgcctcaagaaatgtgtagagag 1500  
Q 1527 CTCTAATTCCTAGAAAGTCCCTGCTTTAGGTATCCACCTCTTCTGCTGAGCA 1586  
D 1501 cctcaatctcaggaagtgctcacttcaaggtcaaccacacctcttctcctgagca 1560  
Q 1587 CTCTGCTTGCACATTAGAG 1607  
D 1561 ctctgctcgcacattagag 1581

RESULT 9  
AAV61989  
ID AAV61989 standard; cDNA: 2162 BP.  
XX  
AC AAV61989;  
XX  
DT 11-JAN-1999 (first entry)  
XX  
DE Human mu-opioid receptor cDNA variant 5.  
XX  
KW Mu-opioid receptor; variant; polymorphism; mutant; detection; disease;  
KW predisposition; addiction; analgesic; anesthetic; anti-addictive;  
KW psychopharmacological agent; diagnostic; side effect; drug; opiate;  
KW cocaine; inherited alcoholism; human; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 213..2040  
FT /tag= a  
FT /product= "mu-opioid receptor"  
FT misc\_feature 502..503  
FT /tag= b  
FT /note= "Site of intron 1"  
FT misc\_feature 855..856  
FT /tag= c  
FT /note= "Site of intron 2"  
FT misc\_feature 1376..1377  
FT /tag= d  
FT /note= "Site of intron 3"  
FT mutation 229  
FT /tag= e  
FT /note= "Wild type C is replaced by T"  
PN MO9833937-A2.  
XX  
XX 06-AUG-1998.  
PD  
XX  
PF 02-FEB-1998; 98MO-DE00382.  
XX  
XX 03-FEB-1997; 97DE-1003925.  
XX

PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
XX  
PI Hoehe M, Mendel B.  
XX  
DR WPI; 1998-437487/37.  
XX  
PT New genomic c and cDNA sequences encoding human mu-opioid receptor -  
PT used, e.g. to predict pre-disposition to addiction and for  
PT development of analgesics, anaesthetics and anti-addiction agents  
XX  
PS Claim 8; Page -: 26pp; German.  
XX  
CC This sequence encodes a novel human mu-opioid receptor in which a C  
CC nucleotide at position 229 of the wild-type sequence represented in  
CC AAV61984 is replaced by an T. The wild-type receptor and its variants,  
CC polymorphisms and mutants are used in a method for detecting  
CC predisposition to disease, particularly addictive disease, by isolating  
CC DNA from a sample, genotyping selected positions and comparing with a  
CC reference DNA. Such sequences are used to develop analgesic,  
CC anaesthetic, anti-addictive and psychopharmacological agents, to construct  
CC genes and vectors, particularly for pharmaceutical development, to  
CC develop diagnostic kits for predicting risk of addiction, response to  
CC analgesics or anaesthetics, or development of side effects from a drug.  
CC Particular applications are to determine risk of addiction to opiates or  
CC cocaine, or of developing inherited alcoholism.  
CC Note: This sequence is not represented in the specification and has  
CC been constructed from the wild-type sequence represented in AAV61984 in  
CC accordance with the specification.  
XX  
XX  
SQ Sequence 2162 BP; 562 A; 564 C; 458 G; 576 T; 2 other;

Query Match 97.0%; Score 1561; DB 19; Length 2162;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 28 TGGGAGGGGGCTATACGAGAGAGAGATGTGATGCTGACCTGGTCCCTCCGCTCGA 87  
DB 1 tgggaagggggtactacagagagagaaatgtaagatgctcagctgctccctccgctga 60  
QY 88 CGCTCTCTCTGTCTAGCCAGGAGCTGTTCTGTAAAGAAACAGAGAGAGTGTGGAGC 147  
DB 61 cgcctctctctgtctacagcagagactggttctgtaagaacaagagagctggtgcagc 120  
QY 148 GCGGAGAGAGAGCGGCTGAGGCGCTTGAGACCGGAAAAAGTCTGCTGCTGCTACT 207  
DB 121 ggcgaagaagcgctgaagcgctggaaccgaaagtctgctctgctact 180  
QY 208 CGGACAGC-GTGGCCGGCGGCGCTGACATGAGACAGAGAGGCTGCCCGCAAGACG 266  
DB 181 cgcacagcggtgcccgcgcgtcagctacatgagacagcgcctgctcccaagacg 240  
QY 267 CCAGCAATTGACATGATGCTTGGCTGATCAATGCTCCCGAGCAAGCCGCGGTT 326  
DB 241 ccagcaattgacatgactgactggtgctgtaactaaagtctcccgacacccgcccgtt 300  
QY 327 CCTGGGTCAACTGTCCCACTTAGATGGCAACTGTCCGACCCATGCGGTCGAACGCA 386  
DB 301 cctgggtcaactgtcccaacttagatggcaactgtccgacccatgctgcgaaccga 360  
QY 387 CCGACCTGGGCGGAGAGACAGCTGTGCTCCGACCGGAGAGTCCCTCATGATCAGG 446  
DB 361 cccacccgtggcggaagacagcctgtgccctccgacccgagctccctcctcaatga 420  
QY 447 CCATCAGATCAGGCGCTCTACTCCATCGTGTGAGGGCTGTCTGGAAATTTCC 506  
DB 421 ccatacagatcagcgccctcaccatcggtgctggtggtggtctccgaaactcc 480  
QY 507 TGGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566  
DB 481 tggatcatgatatgatatgatatgatatgatatgatatgatatgatatgatatgatat 540  
QY 567 TCAACTTGGCTGTGGAGATGCTTACGCAACCACTACCTGCGCTTCAGAGTGTGAAT 626

DB 541 tcaacctgctctgacagatgacctagccaccagttaccctgcccctccagatgtgatat 600  
QY 627 ACCTAATGGGAGACATGGCCATTTTGGACCAATCCCTTTCAGAGATGATGATCCATAT 686  
DB 601 accctaattgggaacatgagcactcttggaacacactcttggaagatagatcccaatga 660  
QY 687 ACTTAACATGTTTCCACAGCATATTTACCCCTTCCACCATGATGATGATGATGATGAT 746  
DB 661 acttaaacatgctacacagatcatccacccctcgcacacatgagtgatgcatacatg 720  
QY 747 CAGTCTGCCACCTCTGTAAGGCTTACATTTCCGTACTCCCGCAATGCCAAATTTATCA 806  
DB 721 cagctctgccacccctgtaagccttagatcttcgctactcccgaaatgccaataatca 780  
QY 807 ATGCTGCACTGATGATCTCTCTCAGCCATTTGGTCTTCCGTAATGATGATGATGATGAT 866  
DB 781 atgctgcaactgatactctctctcctccacatgagctctctctgtaaatgtaactca 840  
QY 867 CAATAACAGGCAAGTTCCATAGATTTGACACTAACATTTCTCATCAACCTGTACT 926  
DB 841 caaataacaggcaagttccatagatgtgtacatacatctctccatccaaactgtact 900  
QY 927 GGGAAACCTGCTGAATCTGTGTTTTCATCTTCCGCTTCATATGCACTGCTCATCA 986  
DB 901 gggaaacctgctgaatctgtgttttcatcttccgcttcataatgacagtgctcatca 960  
QY 987 TTACCGTGTGATGAGACTGATGATTTGGCGCTCAAGAGTGGCCGATGCTCTGCTGCT 1046  
DB 961 ttaccggtgtgatagactgatagtatgactctgacctcaagatgctcgcaatgctctg 1020  
QY 1047 CCAAGAAAGAGAGAGATCTTCGAAGATCACAGATGCTGCTGCTGCTGCTGCTGCTG 1106  
DB 1021 ccaagaagaaagagagatcttccgaagatccacagatggtgtgtgtgtgtgtgtgtgt 1080  
QY 1107 TGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1166  
DB 1081 tgttcacgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1140  
QY 1167 TCCGAGAACTACGTTTCCAGACTGTTTCTTGGGCACTTCTGCTGCTGCTGCTGCTGCT 1226  
DB 1141 tccgagaactagcttccagactgttcttgcgaactctgcatgtgctctagttacaaca 1200  
QY 1227 ACAGCTGCTTCAACCCAGTCTCTTATGATTTTCTGATGAAACTTCAACGATGCTTCA 1286  
DB 1201 acagctgcttcaacccagctcttattgacttctggaatgaacttcaaacgactgttca 1260  
QY 1287 GAGAGTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1346  
DB 1261 gagagtctgtaaccacactcttccaaatgagcaacaaacccacacacacacacacac 1320  
QY 1347 AGAAGACTAGAGACACCCCTCCACGGCCAAATACAGTGAATCAATCAATCAATCAAT 1406  
DB 1321 agaagactagagacacccctccacggccaaatagagtagagtagaactcaatcacagtag 1380  
QY 1407 AAAATCTGGAAGCAGAAATGCTCCGTTGCCCTTACAGGCTTCATGCCACTTCCGACT 1466  
DB 1381 aaatctggaagcagaaatgctccgttgccttaacagggctcctatgcatccttcgac 1440  
QY 1467 CACCAAGCTTGAAGACCAACCATGATGATGAGAGAGTGTCTTCAGAAATGTGAGAGG 1526  
DB 1441 caccaagcttgaagaccaaactgatagtggaagcaggtgtgtccaaagatgtgtagaagg 1500  
QY 1527 CTCTAATTTCTAGGAAGTGCCTGCTTTTATGATCAACCACTTTCTCTCTGGGCA 1586  
DB 1501 ctctaattctctggaagtgactactttagtgaatcaactcttctctctctgcca 1560  
QY 1587 CTCTGCTCTGACATTAGAG 1607  
DB 1561 ctctgctctgacattagagg 1581

RESULT 10

|  |    |                                       |
|--|----|---------------------------------------|
| AAV61990   | ID | AAV61990 standard; cDNA; 2162 BP.     |
| AAV61990;  | AC |                                       |
| 11-JAN-1999 (first entry)  | DT |                                       |
| Human mu-opioid receptor cDNA variant 6.   | DE |                                       |
| Mu-opioid receptor; variant; polymorphism; mutant; detection; disease; predisposition; addiction; analgesic; anaesthetic; anti-addictive; psychopharmaceutical agent; diagnostic; side effect; drug; opiate; cocaine; inherited alcoholism; human; ss. | KW |                                       |
| Homo sapiens.  | OS |                                       |
| Synthetic.   | OS |                                       |
| Key  | FT | Location/Qualifiers                   |
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|  | FT | /*tag= a                              |
|  | FT | /product= "mu-opioid receptor"        |
| misc_feature   | FT | 502..503                              |
|  | FT | /*tag= b                              |
|  | FT | /note= "Site of intron 1"             |
| misc_feature   | FT | 855..856                              |
|  | FT | /*tag= c                              |
|  | FT | /note= "Site of intron 2"             |
| misc_feature   | FT | 1376..1377                            |
|  | FT | /*tag= d                              |
|  | FT | /note= "Site of intron 3"             |
| mutation   | FT | 330                                   |
|  | FT | /*tag= e                              |
|  | FT | /note= "Wild type A is replaced by G" |
| MO9833937-A2.  | XX |                                       |
| 06-AUG-1998.   | PD |                                       |
| 02-FEB-1998; 98MO-DE00382.   | PF |                                       |
| 03-FEB-1997; 97DE-1003925.   | PR |                                       |
| (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.   | XX |                                       |
| Hoehe M, Wendel B;   | PA |                                       |
| WPI: 1998-437487/37.   | PI |                                       |
| New genomic and cDNA sequences encoding human mu-opioid receptor -   | PT |                                       |
| used, e.g. to predict pre-disposition to addiction and for   | PT |                                       |
| development of analgesics, anaesthetics and anti-addiction agents  | PT |                                       |
| Claim 8; Page -: 26pp; German.   | PS |                                       |
| This sequence encodes a novel human mu-opioid receptor in which an A   | CC |                                       |
| nucleotide at position 330 of the wild-type sequence represented in  | CC |                                       |
| AAV61984 is replaced by a G. The wild type receptor and its variants,  | CC |                                       |
| polymorphisms and mutants are used in a method for detecting   | CC |                                       |
| predisposition to disease, particularly addictive disease, by isolating  | CC |                                       |
| DNA from a sample, genotyping selected positions and comparing with a  | CC |                                       |
| reference DNA. Such sequences are used to develop analgesic,   | CC |                                       |
| anaesthetic, anti-addictive and psychopharmaceutical agents, to construct  | CC |                                       |
| genes and vectors, particularly for pharmaceutical development, to   | CC |                                       |
| develop diagnostic kits for predicting risk of addiction, response to  | CC |                                       |
| analgesics or anaesthetics, or development of side effects from a drug.  | CC |                                       |
| Particular applications are to determine risk of addiction to opiates or   | CC |                                       |
| cocaine, or of developing inherited alcoholism.  | CC |                                       |
| Note: This sequence is not represented in the specification and has  | CC |                                       |
| been constructed from the wild-type sequence represented in AAV61984 in  | CC |                                       |
| accordance with the specification.   | CC |                                       |
| Sequence 2162 BP; 561 A; 565 G; 459 G; 575 T; 2 other:   | XX |                                       |

|                       |  |  |            |             |        |
|-----------------------|--|--|------------|-------------|--------|
| Query Match           | 97.0%  | Score 1561   | DB 19      | Length 2162 |        |
| Best Local Similarity | 99.6%  | Pred. No. 0  |            |             |        |
| Matches 1575:         | Conservative   | 0  | Mismatches | 5           | Indels |
|                       |  |  |            |             | Gaps   |
| 1                     |  |  |            |             |        |
| 28                    | TTGGAGAGGGGGCTATTCACGACGAGAGATATTCAGATAGTCCAGCTCGGTCCCTCCGCTGA | 87   |            |             |        |
| DB                    | 1  | ttggagagggggctatcgcagagagagaatgtcagaatgactagctggltccctccgcgttga  | 60         |             |        |
| QY                    | 88   | CGCTCTCTCTGTCTACGCCAGACGTGGTTTCTGTAGAAACACGACGAGCTGTGGCAC        | 147        |             |        |
| DB                    | 61   | cgcctcctctctgtctcagccagagactgttcttgtlaagaacaagacagagactgtgacag   | 120        |             |        |
| QY                    | 148  | GGCGAAAGAACGGGCTGAGGGCGTTTGGCAACCCGAAATCTTCGGGTCTCGGGCTACCT      | 207        |             |        |
| DB                    | 121  | ggcgaaagaaagcggcttgagcgcttgagaccgaaatctcgtgtgccttgcgtacct        | 180        |             |        |
| QY                    | 208  | CGCACAGC-GTCCCGCGCCGGCGCGTACGACATGAGACGACGCGCTGCCACGAAAG         | 266        |             |        |
| DB                    | 181  | cgcacaagcggtgtcccgcccgccgcgtacagtaaccatgtagcaagcagcgctgccccacga  | 240        |             |        |
| QY                    | 267  | CCAGCAATTGCACTGATGCTTGGCGTACTCAAGTTGCTCCCCAGACCCAGCCGGTT         | 326        |             |        |
| DB                    | 241  | ccagcaattgcaactgatgccttgcgttactcaagtgtctccacagaccagccccggtt      | 300        |             |        |
| QY                    | 327  | CCTGGGTCAACTGTGTCGCCCTAGTAAGGACCTGTGCCAGCCATGCGGTCCGGAACCGGA     | 386        |             |        |
| DB                    | 301  | ctctgggtcaactgtgtcccaactlagaatggcagactgttcggaaccaatggtlccgaacgca | 360        |             |        |
| QY                    | 387  | CCGACCTGGGGCGGAGAGACACGCTGTGGCCCTCCGACCGGAGTCCCTCATGATCACGG      | 446        |             |        |
| DB                    | 361  | ccaacctggcgggagagagcagcctgtgacctccgacccgacgtccctccatgatcaagg     | 420        |             |        |
| QY                    | 447  | CCATACACATCATGGCCCTTACTCATGTGTGGTGGGTGGGCTCTTGGGAAATTTCC         | 506        |             |        |
| DB                    | 421  | ccatcacagatccttgccctctactccatcatgtgtggtgtggtggtccttcggaacttcc    | 480        |             |        |
| QY                    | 507  | TGGTATGATGATGATTTGTTCAGATACACCAACAGTGAAGACTCCCAACATCTACATTT      | 566        |             |        |
| DB                    | 481  | tgtcatatgtatgtatgtatgtcagataaccaagaatgaagactctgcaccaatctacatt    | 540        |             |        |
| QY                    | 567  | TCACCTTCCTCTGGCAGATGCTCTTAGCCACCAAGTACCTGCCCTTCCAGAGTGTCAATT     | 626        |             |        |
| DB                    | 541  | tcaaccttctctcttggtcagatgtcctttagccacacagtaacctgtcccttcagagtgtaat | 600        |             |        |
| QY                    | 627  | ACCTATGGAACATGAGCCATTGTGGAACATTCCTTTGCAAGATAGTCAATCCATGATT       | 686        |             |        |
| DB                    | 601  | acctaatgggaacatggtccatttggaaacataccttgcagaagatagtatctccatagatt   | 660        |             |        |
| QY                    | 687  | ACTATTAACATGTTCCACGACATATTCACCTCTGCACCATGAGTGTGATCGATATCATTTG    | 746        |             |        |
| DB                    | 661  | actataaacatgttccaccagacataatcaacctctgcacacatgagtgtltagatagatcgt  | 720        |             |        |
| QY                    | 747  | CAGTGTGGCACCCCTGTCAAGGGCTTAAAGATTTCGTACCTCCCGGAATGCAAAATTAATCA   | 806        |             |        |
| DB                    | 721  | cagtcctgcacccgttccaaggtcccttagatttccgttactcccgaaatgccccaaatlaaca | 780        |             |        |
| QY                    | 807  | ATGTCGTCAACTGATCCCTCTTACAGCCATTGAGTCTTCTGTAAATGTTCAATGGCTACAA    | 866        |             |        |
| DB                    | 781  | atgtctgcgaactgagatcctctcttcaagccattgtcttccgtlaatgtlcatgctacaac   | 840        |             |        |
| QY                    | 867  | CAAAATACAGGCAAGTTTCATAGATTGTACACTTAACATTTCTCATTCACACTGGTACT      | 926        |             |        |
| DB                    | 841  | caaaatacaggaagttlcatagatgttacaactaaacttcttcaatccaaactgttact      | 900        |             |        |
| QY                    | 927  | GGGAAACCTGGTGAAGATCTGTGTTTATCTGTGCCCTTCAATTATGACAGTGCATCA        | 986        |             |        |
| DB                    | 901  | gggaaaacctgttgaaagatctgttlttcatcttgcgccttaattatgcagtgctacaca     | 960        |             |        |
| QY                    | 987  | TTACCGTGTGTTATGAGCATGATCTTGCGCTCAAGAGTCCGACATGCTCTGTGCT          | 1046       |             |        |
| DB                    | 961  | ttaccctgtgtcatatgacatgacatcttccgctccaaggttcccaatgctctcgtcgt      | 1020       |             |        |









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 FT misc\_feature 855..856  
 FT /tag= C  
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 FT /note= "Site of intron 3"  
 FT mutation 1014  
 FT /tag= e  
 FT /note= "Wild type T is replaced by C"  
 PN W09833937-A2.  
 XX 06-AUG-1998.  
 XX 02-FEB-1998; 98WO-DE00382.  
 XX 03-FEB-1997; 97DE-1003925.  
 PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.  
 PI Hoehe M, Wendel B;  
 DR WPI; 1998-437487/37.  
 PT New genomic and cDNA sequences encoding human mu-opioid receptor -  
 PT used, e.g. to predict pre-disposition to addiction and for  
 PT development of analgesics, anaesthetics and anti-addiction agents  
 PS  
 XX Claim 8; Page -: 26pp; German.  
 CC This sequence encodes a novel human mu-opioid receptor in which a T  
 CC nucleotide at position 1014 of the wild-type sequence represented in  
 CC AA61984 is replaced by a C. The wild type receptor and its variants,  
 CC polymorphisms and mutants are used in a method for detecting  
 CC predisposition to disease, particularly addictive disease, by isolating  
 CC DNA from a sample, genotyping selected positions and comparing with a  
 CC reference DNA. Such sequences are used to develop analgesic,  
 CC anesthetic, anti-addictive and psychopharmaceutical agents, to construct  
 CC genes and vectors, particularly for pharmaceutical development, to  
 CC develop diagnostic kits for predicting risk of addiction, response to  
 CC analgesics or anaesthetics, or development of side effects from a drug.  
 CC Particular applications are to determine risk of addiction to opiates or  
 CC cocaine, or of developing inherited alcoholism.  
 CC Note: This sequence is not represented in the specification and has  
 CC been constructed from the wild-type sequence represented in AA61984 in  
 CC accordance with the specification.  
 XX  
 XX  
 SQ Sequence 2162 BP: 562 A: 566 C: 458 G: 574 T: 2 other:

Query Match 97.0%; Score 1561; DB 19; Length 2162;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1575; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
 Oy 28 TGGGAGGGGCGATACGAGAGAGATGTCAGATCGATCGGTCGCCCGCGCTGA 87  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2002, 21:04:38 : Search time 92.08 Seconds  
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Title: US-08-305-518-7

Perfect score: 1610  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 14         | 443.2  | 27.5        | 1829   | 4     | US-08-387-707-7   |
| 15         | 443.2  | 27.5        | 2272   | 3     | US-08-147-592A-3  |
| 16         | 434.8  | 27.0        | 1142   | 3     | US-08-765-743-1   |
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| 26         | 356.4  | 22.1        | 1452   | 1     | US-08-149-093A-3  |
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| 35 | 199.4 | 12.4 | 1351 | 1 | US-07-816-283-5  | Sequence 5, Appl1  |
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#### ALIGNMENTS

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RESULT 1
US-08-889-108-7
: Sequence 7, Application US/08889108
: Patent No. 6103492
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: GENERAL INFORMATION:
: APPLICANT: Yu, Lei
: TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P. O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/889,108
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/305,518
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Wilson, Mark B.
: REGISTRATION NUMBER: 37,259
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512-418-3000
: TELEFAX: 512-474-7577
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1610 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-889-108-7
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Query Match 100.0%; Score 1610; DB 3; Length 1610;  
Best local similarity 100.0%; Pred. No. 0;  
Matches 1610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 APPLICANT:  
 TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P. O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/10358  
 FILING DATE: Concurrently herewith  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/120,601  
 FILING DATE: 13 SEPTEMBER 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WILSON, MARK B.  
 REGISTRATION NUMBER: 37,259  
 REFERENCE/DOCKET NUMBER: INDA005P--  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (512) 418-3000  
 TELEFAX: (713) 789-2679  
 TELEX: 79-0924  
 INFORMATION FOR SEO ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1610 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single

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;      TOPOLOGY:  linear
;      MOLECULE TYPE:  CDNA
PCT-US94-10358-7

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| Best Local Similarity | 100.0%          | Pred. No. 0;  |           |              |
| Matches 1610;         | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0;      |

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| QY | 121 | GTAAGAAACACACAGAGCTGTGGCAGGGGAAAGGAAAGGGGCTGAGGGCTTGGAAACC     | 180 |
| Db | 121 | GTAAGAAACACACAGAGCTGTGGCAGGGGAAAGGAAAGGGGCTGAGGGCTTGGAAACC     | 180 |
| QY | 181 | GAAAGATCTCGGTCTCTGGCTACTGCAACAGCTGGCCCGCCGCGCTCAGTATACAT       | 240 |
| Db | 181 | GAAAGATCTCGGTCTCTGGCTACTGCAACAGCTGGCCCGCCGCGCTCAGTATACAT       | 240 |
| QY | 241 | GGACAGCAGCGCTGCCCCCAGCAAGCGCAGCAATTGCATGATGCGCTTGGCGTACTCAAG   | 300 |
| Db | 241 | GGACAGCAGCGCTGCCCCCAGCAAGCGCAGCAATTGCATGATGCGCTTGGCGTACTCAAG   | 300 |
| QY | 301 | TTTGCTCCCGCAGCACCAGCCCGGTCTCTGGGTCACTTGTCCACTTAAATGGCAACT      | 360 |
| Db | 301 | TTTGCTCCCGCAGCACCAGCCCGGTCTCTGGGTCACTTGTCCACTTAAATGGCAACT      | 360 |
| QY | 361 | GTCCGACCCATGCGGTCCGGAAGCCGACACGACCTGGGCGGAGACAGCCTGTGCCCCCTC   | 420 |
| Db | 361 | GTCCGACCCATGCGGTCCGGAAGCCGACACGACCTGGGCGGAGACAGCCTGTGCCCCCTC   | 420 |
| QY | 421 | GACCGGCGAGTCCCTCATGATCAGGGCCATCAGCATGAGCCCTTACTACCATCTGTGTG    | 480 |
| Db | 421 | GACCGGCGAGTCCCTCATGATCAGGGCCATCAGCATGAGCCCTTACTACCATCTGTGTG    | 480 |
| QY | 481 | CGTGGTGGGGCTCTTGGGAACTTCTGTGTCATGTATGTATTTGATGATACACCAAGAT     | 540 |
| Db | 481 | CGTGGTGGGGCTCTTGGGAACTTCTGTGTCATGTATGTATTTGATGATACACCAAGAT     | 540 |
| QY | 541 | GAAAGCTGCCCAACAACATCAATTTTCAACCTTGGCTGGCAGATGCCCTTACGCCACAG    | 600 |
| Db | 541 | GAAAGCTGCCCAACAACATCAATTTTCAACCTTGGCTGGCAGATGCCCTTACGCCACAG    | 600 |
| QY | 601 | TACCCCTGCCCTTCCAGAGTGTGAATTAACATAATGGCAACATGGCCATTGGCAACATCTCT | 660 |
| Db | 601 | TACCCCTGCCCTTCCAGAGTGTGAATTAACATAATGGCAACATGGCCATTGGCAACATCTCT | 660 |
| QY | 661 | TTGCAAGATAGTATGTCTCCATAGATTACTATAACATTTCAACAGCATATTCAACCCCTCTG | 720 |
| Db | 661 | TTGCAAGATAGTATGTCTCCATAGATTACTATAACATTTCAACAGCATATTCAACCCCTCTG | 720 |
| QY | 721 | CACCATGAGTGTATGATGATTAATTTGAGTGTGCAACCTGCAAGGCCCTTAATTTCCG     | 780 |
| Db | 721 | CACCATGAGTGTATGATGATTAATTTGAGTGTGCAACCTGCAAGGCCCTTAATTTCCG     | 780 |
| QY | 781 | TACTGCCCGGAAATGCCAAAATTTATCAATGTCTGCAACGTGATCCTCTCTCAGCCATTGG  | 840 |
| Db | 781 | TACTGCCCGGAAATGCCAAAATTTATCAATGTCTGCAACGTGATCCTCTCTCAGCCATTGG  | 840 |
| QY | 841 | TCCTTCCTGTAAATGTTCAATGCGTACACAAATAATACAGCAAGGTTCATATGTTGACT    | 900 |
| Db | 841 | TCCTTCCTGTAAATGTTCAATGCGTACACAAATAATACAGCAAGGTTCATATGTTGACT    | 900 |
| QY | 901 | AACATTCCTCATATCAACCTGTGTAAGTGGGAAACCTGTCTGAACATCTGTCTTTCATCTT  | 960 |
| Db | 901 | AACATTCCTCATATCAACCTGTGTAAGTGGGAAACCTGTCTGAACATCTGTCTTTCATCTT  | 960 |

|  |      |   |      |
|--|------|---|------|
| OY   | 961  | CGCCCTGATTATWGCACAGTGCCTGCATCAATTAACCGGTCTCTATGGACGTAGATCAATTCGCGCT | 1020 |
| OY   | 961  | CGCCCTGATTATWGCACAGTGCCTGCATCAATTAACCGGTCTCTATGGACGTAGATCAATTCGCGCT | 1020 |
| Db   | 961  | CGCCCTGATTATWGCACAGTGCCTGCATCAATTAACCGGTCTCTATGGACGTAGATCAATTCGCGCT | 1020 |
| OY   | 1021 | CAAGAGTGTCCGCTGCTCTCTGCTCCCAAAAGAGAGAGAAAGCAAGAAATCTTGCAGAGATCAC    | 1080 |
| Db   | 1021 | CAAGAGTGTCCGCTGCTCTCTGCTCCCAAAAGAGAGAGAAAGCAAGAAATCTTGCAGAGATCAC    | 1080 |
| OY   | 1081 | CAGATGGTGTGCTGT   | 1140 |
| Db   | 1081 | CAGATGGTGTGCTGT   | 1140 |
| OY   | 1141 | CGTATCATTTAAACCCCTTGGTTTCAMTCCCAAGAAATACAGTTCACAGACGTTCCTTGGCA      | 1200 |
| Db   | 1141 | CGTATCATTTAAACCCCTTGGTTTCAMTCCCAAGAAATACAGTTCACAGACGTTCCTTGGCA      | 1200 |
| OY   | 1201 | CTTCTGCATTTGCTCTAGTGTACACAAACAGCTCCCAACCCAGTCTTTATGATCTTCT          | 1260 |
| Db   | 1201 | CTTCTGCATTTGCTCTAGTGTACACAAACAGCTCTTCTATCCCAACCTCTTCCAAATCTTGA      | 1320 |
| OY   | 1261 | GGATGAAAACTTCAAAAGATGCTTCAGAGAGTCTCTATCCCAACCTCTTCCAAATCTTGA        | 1320 |
| Db   | 1261 | GGATGAAAACTTCAAAAGATGCTTCAGAGAGTCTCTATCCCAACCTCTTCCAAATCTTGA        | 1320 |
| OY   | 1321 | GCAACAAAACTCCACTGATTTGTGTGACAGAACATAGAGACACCCCTCCAGGCGCAATAC        | 1380 |
| Db   | 1321 | GCAACAAAACTCCACTGATTTGTGTGACAGAACATAGAGACACCCCTCCAGGCGCAATAC        | 1380 |
| OY   | 1381 | AGTGGATAGAACTATATCATATGAGTGTAGAAAATCTGGAAGACAGAACTGCTCGTTCCTTA      | 1440 |
| Db   | 1381 | AGTGGATAGAACTATATCATATGAGTGTAGAAAATCTGGAAGACAGAACTGCTCGTTCCTTA      | 1440 |
| OY   | 1441 | ACAGGGTCTCATGCTCCATTTCCGACCTTCACCAAGCTTAGAAGCCACCATATGATGTGAAGC     | 1500 |
| Db   | 1441 | ACAGGGTCTCATGCTCCATTTCCGACCTTCACCAAGCTTAGAAGCCACCATATGATGTGAAGC     | 1500 |
| OY   | 1501 | AGGTTGCTTCAAGATGTGTAGAGAGGCTCTAATTTCTTAGGAAAGTGCTGCTTTAGGT          | 1560 |
| Db   | 1501 | AGGTTGCTTCAAGATGTGTAGAGAGGCTCTAATTTCTTAGGAAAGTGCTGCTTTAGGT          | 1560 |
| OY   | 1561 | CATCCAACTCTTCTCTCTCTGCGCACTGCTGCTGCAATAGAGGCGG                      | 1610 |
| Db   | 1561 | CATCCAACTCTTCTCTCTCTGCGCACTGCTGCTGCAATAGAGGCGG                      | 1610 |
| RESULT 3   |      |   |      |
| US-08-188-275A-1   |      |   |      |
| ; Sequence 1, Application US/08188275A                                 |      |   |      |
| ; Patent No. 6258556   |      |   |      |
| ; GENERAL INFORMATION:   |      |   |      |
| ; APPLICANT: Uhl, George R.  |      |   |      |
| ; APPLICANT: Wang, Jia-Bel   |      |   |      |
| ; APPLICANT: Johnson, Peter S.   |      |   |      |
| ; APPLICANT: Persico, Antonio  |      |   |      |
| ; TITLE OF INVENTION: cDNA and Genomic Clones Encoding Human           |      |   |      |
| ; TITLE OF INVENTION: Mu Opiate Receptor and the Purified Gene Product |      |   |      |
| ; NUMBER OF SEQUENCES: 12  |      |   |      |
| ; CORRESPONDENCE ADDRESS:  |      |   |      |
| ; ADDRESSEE: Birch, Stewart, Kolasch & Birch                           |      |   |      |
| ; STREET: P.O. Box 747   |      |   |      |
| ; CITY: Falls Church   |      |   |      |
| ; STATE: Virginia  |      |   |      |
| ; COUNTRY: USA   |      |   |      |
| ; ZIP: 22040-3487  |      |   |      |
| ; COMPUTER READABLE FORM:  |      |   |      |
| ; MEDIUM TYPE: Floppy disk   |      |   |      |
| ; COMPUTER: IBM PC compatible  |      |   |      |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS                                      |      |   |      |
| ; SOFTWARE: PatentIn Release #1.0, Version #1.25                       |      |   |      |
| ; CURRENT APPLICATION DATA:  |      |   |      |
| ; APPLICATION NUMBER: US/08/188,275A                                   |      |   |      |
| ; FILING DATE: 28-Jan-1994   |      |   |      |
| ; CLASSIFICATION: 530  |      |   |      |

ATTORNEY/AGENT INFORMATION:  
 NAME: Murphy Jr., Gerald M.  
 REGISTRATION NUMBER: 28,977  
 REFERENCE/DOCKET NUMBER: 1173-449P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-241-1300  
 TELEFAX: 703-241-2848  
 TELEX: 248345  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2160 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: -  
 LOCATION: 1..2160 /label= cDNA  
 OTHER INFORMATION: /note= "cDNA encoding human mu opiate receptor"  
 US-08-188-275A-1

Query Match 96.5%; Score 1553; DB 4; Length 2160;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1567; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 36 GGCATACGAGAGAGAAATGTGATGCTCAGCTGGTCCCGCGCGCTGACGCTCCTC 95  
 DB 9 GGCATATGAGAGAGAGAAATGTGATGCTCAGCTGGTCCCGCGCGCTGACGCTCCTC 68  
 QY 96 TCTGTCTCAGCCAGAGAGCTGTTCTGTAGAAACAGCAGAGAGCTGTGGCAGCGCGAAG 155  
 DB 69 TCTGTCTCAGCCAGAGAGCTGTTCTGTAGAAACAGCAGAGAGCTGTGGCAGCGCGAAG 128  
 QY 156 GAAGCGGCTGAGGCGCTTGGAAACCCGAAAGTCTCGGTGCTCCTGGGTACTCTGGCAGAC 215  
 DB 129 GAAGCGGCTGAGGCGCTTGGAAACCCGAAAGTCTCGGTGCTCCTGGGTACTCTGGCAGAC 188  
 QY 216 -GTGCGCGCGCGCGCTGATACCTGACAGCAGCGCTCCCGCAGCAAGCGCAGCAAT 274  
 DB 189 GGTGCGCGCGCGCGCTGATACCTGACAGCAGCGCTCCCGCAGCAAGCGCAGCAAT 248  
 QY 275 TGCACGTGATGCTTGGCGTACTCAAGTCTCCCGACGACCCGCGGTCTCTGGGTC 334  
 DB 249 TGCACGTGATGCTTGGCGTACTCAAGTCTCCCGACGACCCGCGGTCTCTGGGTC 308  
 QY 335 AACCTGTCACCTTAGATGCAACCTGTGCGACCGCATGGGTCGGAACCGCACCGACCTG 394  
 DB 309 AACCTGTCACCTTAGATGCAACCTGTGCGACCGCATGGGTCGGAACCGCACCGACCTG 368  
 QY 395 GGGGAGAGACAGCCTGTGCTCCGACCGGAGAGTCCCTGCATGATCAGGGCATTACG 454  
 DB 369 GGGGAGAGACAGCCTGTGCTCCGACCGGAGAGTCCCTGCATGATCAGGGCATTACG 428  
 QY 455 ATCATGGCCCTCTACTCTCATCTGCTGCTGGTGGGCTCTTGGAAACTCTGCTGTCAG 514  
 DB 429 ATCATGGCCCTCTACTCTCATCTGCTGCTGGTGGGCTCTTGGAAACTCTGCTGTCAG 488  
 QY 515 TATGTGATTTGTCAGATACCAAGATGAAGTGGCCCAACCATCTACATTTTCAACCTT 574  
 DB 489 TATGTGATTTGTCAGATACCAAGATGAAGTGGCCCAACCATCTACATTTTCAACCTT 548  
 QY 575 GCTTGGCAGATGCTTAGCCACAGTACCTGCTCCCTTCCAGAGTGTGAATTAATG 634  
 DB 549 GCTTGGCAGATGCTTAGCCACAGTACCTGCTCCCTTCCAGAGTGTGAATTAATG 608  
 QY 635 GGAACATGGCATTGGAAACCATCTTTCGAAGATAGTATCTCCATAGTATCTATAC 694  
 DB 609 GGAACATGGCATTGGAAACCATCTTTCGAAGATAGTATCTCCATAGTATCTATAC 668  
 QY 695 ATGTACACGAGATATTCACCCCTCTGACCATAGTGTATGATACATTTGAGCTGTC 754

DB 669 ATGTACACGAGATATTCACCCCTCTGACCATCATAGTGTGATGATACATTCGAGCTGTC 728  
 QY 755 CACCGTGTCAAGGCTTAGATTTCCGACTCCCGGAAATGCCAAATTTATCAATGTCTGC 814  
 DB 729 CACCGTGTCAAGGCTTAGATTTCCGACTCCCGGAAATGCCAAATTTATCAATGTCTGC 788  
 QY 815 AACGTGATCTCTCTTCCAGCATTTGGTCTCTGTATGATTTTCAAGCAAAATAC 874  
 DB 789 AACGTGATCTCTCTTCCAGCATTTGGTCTCTGTATGATTTTCAAGCAAAATAC 848  
 QY 875 AGGCAAGTTCATATGATTTTACATACATTTCTGTATCAACCTGTGATGGAAGAC 934  
 DB 849 AGGCAAGTTCATATGATTTTACATACATTTCTGTATCAACCTGTGATGGAAGAC 908  
 QY 935 CTGCTGAGATGCTGTGTTTTCATCTTCCGCTTCAATATGACAGTGGTCAATTAACGTC 994  
 DB 909 CTGCTGAGATGCTGTGTTTTCATCTTCCGCTTCAATATGACAGTGGTCAATTAACGTC 968  
 QY 995 TGTATGAGTATGATCTTTCGCTCAAGAGTGTCCGATGCTCTGCTGCTCCAAAGAA 1054  
 DB 969 TGTATGAGTATGATCTTTCGCTCAAGAGTGTCCGATGCTCTGCTGCTCCAAAGAA 1028  
 QY 1055 AAGGACAGCATCTTTCGAGAGATCACAGAGATGCTGCTGCTGCTGCTGCTGCTGCT 1114  
 DB 1029 AAGGACAGCATCTTTCGAGAGATCACAGAGATGCTGCTGCTGCTGCTGCTGCTGCT 1088  
 QY 1115 GTCTGCTGAGCTCCCATTCATTTACATTTAGTCATTTAAAGCCCTTGGTTCAATCCAGAA 1174  
 DB 1089 GTCTGCTGAGCTCCCATTCATTTACATTTAGTCATTTAAAGCCCTTGGTTCAATCCAGAA 1148  
 QY 1175 ACTAGCTTCAGACTGTTCTTGGCACTTCTGCAATTCCTAGATTACAAACACAGCTG 1234  
 DB 1149 ACTAGCTTCAGACTGTTCTTGGCACTTCTGCAATTCCTAGATTACAAACACAGCTG 1208  
 QY 1235 CTCACCCAGTCTTTATGATTTCTGAGTGAAGTCAAAAGTCTTCAAGAGTCTTCAAGAGTTC 1294  
 DB 1209 CTCACCCAGTCTTTATGATTTCTGAGTGAAGTCAAAAGTCTTCAAGAGTCTTCAAGAGTTC 1268  
 QY 1295 TGTATCCCAACCTCTTCCAAATTTGAGAGCAAAACCTGCACTGATTTGCTGAGACACT 1354  
 DB 1269 TGTATCCCAACCTCTTCCAAATTTGAGAGCAAAACCTGCACTGATTTGCTGAGACACT 1328  
 QY 1355 AGAGACACCCCTTCCAGGCGCAATACAGTGTGATGAACATATATGACTAGAAATCTG 1414  
 DB 1329 AGAGACACCCCTTCCAGGCGCAATACAGTGTGATGAACATATATGACTAGAAATCTG 1388  
 QY 1415 GAAGCAGAAACCTGCTCGTGGTCCCTTAACAGAGGCTCATGCAATTCGACCTTACCAAGC 1474  
 DB 1389 GAAGCAGAAACCTGCTCGTGGTCCCTTAACAGAGGCTCATGCAATTCGACCTTACCAAGC 1448  
 QY 1475 TTGAAGCCACCATGTATGTGAAGCAGGTTGCTTCAAGAAATGTGAGAGGCTCTAATT 1534  
 DB 1449 TTGAAGCCACCATGTATGTGAAGCAGGTTGCTTCAAGAAATGTGAGAGGCTCTAATT 1508  
 QY 1535 CTCTAGGAAAGTCTGCTTTTATGATCAACCTTTCTCTCTGAGCACTGCTGTC 1594  
 DB 1509 CTCTAGGAAAGTCTGCTTTTATGATCAACCTTTCTCTCTGAGCACTGCTGTC 1568  
 QY 1595 TGCACATTTAGAG 1607  
 DB 1569 TGCACATTTAGAG 1581

RESULT 4  
 US-08-889-108-1  
 Sequence 1, Application US/08889108  
 Patent No. 6103492  
 GENERAL INFORMATION:  
 APPLICANT: Yu, Lei  
 TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee





QY 1406 GAAATCTGGAAGCAAACTGCTCCGTTGCCCTAAACAGGCTCATGCCATTCCGACCT 1465  
 DB 1375 GAAATCTGGAAGCAAACTGCTCCGTTGCCCTAAACAGGCTCATGCCATTCCGACCT 1434  
 QY 1466 TCACCAAGCTTAGAAGCCAGCATGTATGTGAAGCAGGTTGCTTCAGAAATGTGAGAG 1525  
 DB 1435 TCAGTAAGCTTAGAAGCCAGCATGTATGTGAAGCAGGTTGCTTCAGAAATGTGAGAG 1494  
 QY 1526 GCTCAATCTCTAGGAAGTCCCTGCTTTAGGTCATCCCAACCTCTTCTCTGAGCC 1585  
 DB 1495 GCTCAATCTCTAGGAAGTCCCTGCTTTAGGTCATCCCAACCTCTTCTCTGAGCC 1551  
 QY 1586 ACTGCTCTGCAATTTAGAG 1606  
 DB 1552 ACTGCTCTGCAATTTAGAG 1572

RESULT 6  
 US-08-120-601B-1  
 : Sequence 1, Application US/08120601B  
 : Patent No. 6235496  
 : GENERAL INFORMATION:  
 : APPLICANT: Yu, Lei  
 : TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND  
 : NUMBER OF INVENTIONS: METHODS  
 : NUMBER OF SEQUENCES: 9  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Arnold, White & Durkee  
 : STREET: P.O. Box 4433  
 : CITY: Houston  
 : STATE: Texas  
 : COUNTRY: USA  
 : ZIP: 77210  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/120,601B  
 : FILING DATE: 13-SEP-1993  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Wilson, Mark B.  
 : REGISTRATION NUMBER: 37,259  
 : REFERENCE/DOCKET NUMBER: INDA:002  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 512/418-3000  
 : TELEFAX: 512/474-7577  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1618 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : FEATURE:  
 : NAME/KEY: CDS  
 : LOCATION: 214..1407  
 : US-08-120-601B-1

Query Match 69.8%; Score 1123.8; DB 4; Length 1618;  
 Best Local Similarity 83.7%; Pred. No. 3e-290;  
 Matches 123; Conservative 0; Mismatches 247; Indels 11; Gaps 4;

QY 27 GTGGAGGGGCTATACGAGAGAGATGTAGATGCTCAGCTGGTCCCTCGCGCTG 86  
 DB 2 GTGGAGGGGCTATACGAGAGAGATGTAGATGCTCAGCTGGTCCCTCGCGCTG 60  
 QY 87 AGCGTCTCTGTCTCACCAGGAGTGTCTTCTGTAAGAAACAGCAGAG-CTGTGGA 145  
 DB 61 CGGCTCTCTGTCTCACCAGGAGTGTCTTCTGTAAGAAACAGCAGAG-CTGTGGA 120

QY 146 GCGGGAAGAGAGGCTGAGGCGCTTGGAAACCCGAAAGTCTCGGTCTCTGCTAC 205  
 DB 121 GCTGTGAGAGAGAGAGGCTGAGGCGCTTGGAAACCCGAAAGTCTCGGTCTCTGCTAC 180  
 QY 206 CTGCGACAGCGTGGCCCGCCGCTCACTACCATGAGCAGGCGTCCCGCAAGC 265  
 DB 181 ACCTACCTAGTACGAGGCTTCAAGCAGCATGAGCAGGCGTCCCGCAAGC 240  
 QY 266 GCGACCAATTTGACATGATGCTTGGCTTCACTACCATGAGCAGGCGTCCCGCAAGC 325  
 DB 241 ACCAGGAGCTGTGACAGCCCTTACCTGAGCAAGTGTCTCCCGCAAGC 294  
 QY 326 TCCCTGAGTCACTTCTCCCTTACCTGAGCAAGTGTCTCCCGCAAGC 385  
 DB 295 TCCCTGAGTCACTTCTCCCTTACCTGAGCAAGTGTCTCCCGCAAGC 354  
 QY 386 ACCGACCTGGGCGGAGAGACAGCTGTGCTCCGAGCGGAGTCTCCATGATCAGC 445  
 DB 355 ACCGACCTGGGCGGAGAGACAGCTGTGCTCCGAGCGGAGTCTCCATGATCAGC 414  
 QY 446 GCGATCAGCATGATGCGCTTCTACTTCATGCTGTGCTGTGGGCTCTTGGAAACTTC 505  
 DB 415 GCGATCAGCATGATGCGCTTCTACTTCATGCTGTGCTGTGGGCTCTTGGAAACTTC 474  
 QY 506 CTGTCATGTATGTGATTTGTACATACACCAAGATGAAGACGACCAACATCTACAT 565  
 DB 475 CTGTCATGTATGTGATTTGTACATACACCAAGATGAAGACGACCAACATCTACAT 534  
 QY 566 TTCAACCTTGTCTGTGAGAGTCTTACGACAGCTTACGACAGTCTTGTGAGAGTGAAT 625  
 DB 535 TTCAACCTTGTCTGTGAGAGTCTTACGACAGTCTTACGACAGTCTTGTGAGAGTGAAT 594  
 QY 626 TACCTAATGGAAGATGAGCATTTGGAACCATCTTGTGGAAGTGTGATTCGCAATGAT 685  
 DB 595 TACCTAATGGAAGATGAGCATTTGGAACCATCTTGTGGAAGTGTGATTCGCAATGAT 654  
 QY 686 TACTATACATGTTTACACGATATTTACACCTCTGACCATGAGTGTGATGATGAT 745  
 DB 655 TACTATACATGTTTACACGATATTTACACCTCTGACCATGAGTGTGATGATGAT 714  
 QY 746 GCAAGTCTGACCGCTGTGAGGCTTGAATTTCCGATCTCCCGCAAGTGTGATGAT 805  
 DB 715 GCAAGTCTGACCGCTGTGAGGCTTGAATTTCCGATCTCCCGCAAGTGTGATGAT 774  
 QY 806 AATGCTGCAAGTGTGATCTCTGACCATGATTTGCTCTGATGATGATGATGAT 865  
 DB 775 AATGCTGCAAGTGTGATCTCTGACCATGATTTGCTCTGATGATGATGATGAT 834  
 QY 866 ACATAATACAGGAGGTTCCATAGATTTGATACATTAATTTCTCATCAACCTGATAC 925  
 DB 835 ACATAATACAGGAGGTTCCATAGATTTGATACATTAATTTCTCATCAACCTGATAC 894  
 QY 926 TGGGAAACCTGCTGAGATCTGTGTTTTCATCTTCCCTTATATGACAGTCTGATC 985  
 DB 895 TGGGAAACCTGCTGAGATCTGTGTTTTCATCTTCCCTTATATGACAGTCTGATC 954  
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 DB 1075 GTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1134  
 QY 1166 ATCCAGAAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1225  
 DB 1135 ATCCAGAAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1194



[illegible]

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RESULT 7
US-08-120-601B-3
Sequence 3, Application US/08120601B
Patent No. 6235496
GENERAL INFORMATION:
APPLICANT: Yu, Lei
TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/120,601B
FILING DATE: 13-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INDA:002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 339..1232
US-08-120-601B-3

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|----------------------------|--------|-------------------|------------|--------------|
| Query Match                | 69.8%; | Score 1123.8;     | DB 4;      | Length 1618; |
| Best Local Similarity      | 83.7%; | Pred. No. 3e-290; |            |              |
| Matches 1323; Conservative | 0;     | Mismatches 247;   | Indels 11; | Gaps 4;      |

|    |      |   |      |
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| OY | 27   | GTGGGAGGGGGCTTTACGAGAGAGAAATTCAGATGCTACGCTGGTCCCTCGCCCTG          | 86   |
| Db | 2    | GTGGAGGGGGCTCAAGCAGAGAGAAATTCAGACGCTCAGA - GCTTCCTCTTGCCCTG       | 60   |
| OY | 87   | ACGCTCCTCTCTGCTCAGCCAGGACTGGTTTCTGTAAAGAACAGCAGAG - CTTGGCA       | 145  |
| Db | 61   | CCGGCTCTTCTTGTTTCCACTAGAGGGCTGTCATGTAAAAATCTGACAGAGGCTAGGGCA      | 120  |
| OY | 146  | GGCGGAGAAAGAAACGGGCTAGAGCGGCTGTGGAAACCCAAAGTCTGGTGTGCTAGCTAC      | 205  |
| Db | 121  | GCTGTGAGAGAGAAAGGCTTGGGGCGCTGTGAAACCCAAAGTCTGAGTGTCTTCAGATTAC     | 180  |
| OY | 206  | CTCGCAGAGCGTGGCCGCGCCGGCCGTGATGACATGAGAGAGCGGTGCCCCAGAAC          | 265  |
| Db | 181  | AGGCTACCTATGTCGAGCAGAGCGCTTCAGACCATGAGCAGCAGCAGCGCCAGGAAAC        | 240  |
| OY | 266  | GGCAGCAATTGCACTGATGCTTGGGCTACTCAAGTTGTTCCCGCAGCACCCAGCCCGGT       | 325  |
| Db | 241  | ACCGAGCAAGCTGTAGACCCCTTAGCTCAGGCAAGTGGTCTCCACACA - - - - - CTTGGC | 294  |
| OY | 326  | TTCGCGGCTCAACTGTCTCCACTTAGATAGTGGAAACCTTCCGACCATGCGGTCGGAACGC     | 385  |
| Db | 295  | TTCGTGGCTCAACTTGTGCCACGTTGATGGGACACCAATCCGATTCACGCGGTGGAACGC      | 354  |
| OY | 386  | ACCGACCTGGGGGGAGAGACAGCCTGTGCGCTCGCAGCGGAGTCCCTCATGTATCAG         | 445  |
| Db | 355  | ACCGGGGCTTGGCGGGAACGACAGCCTGTGCGCTCAGAACCGGACGCGCTTCATGTGTACA     | 414  |
| OY | 446  | GGCATACAGATCAGGGCCCTCTACTCATGATGTGGGTGGTGGGGGTCTTGGAAGATTC        | 505  |
| Db | 415  | GCCATTACCATATGAGCCCTCTACTCTATGCTGTGTGTGTGTGGGCTCTTGGGAAATTC       | 474  |
| OY | 506  | CTGGTCATGATGTGATTTGTCAAGATACACCAGATGAAGACTGCCACCAATCTACATT        | 565  |
| Db | 475  | CTGGTCATGATGTGATTTGATGAATACACAAATGAAGACTGCCACCAATCTACATT          | 534  |
| OY | 566  | TTTCAACCTTGTCTGTGGAGATGCCCTTAAGCCACAGTACCTTGCCTTCAGAGTGTGAT       | 625  |
| Db | 535  | TTTCAACCTTGTCTGTGGAGAGCGCTTAAGGACACAGTACCTCCCTTTCAGATGTCTAC       | 594  |
| OY | 626  | TACCTAATGGGAACATGATGCCATTTTGGAACCATCTTTGGAAATAGTGTATCCATTAAT      | 685  |
| Db | 595  | TACCTGATGGGAACATGAGCCCTTCGGAACATCTCTTGGAAATGTGATTTCAATTAAT        | 654  |
| OY | 686  | TACTATACATGTTCAACAGCATATTACCCCTGTGCACCATGAGTTGATGATACATT          | 745  |
| Db | 655  | TACTATACATGTTCAACAGCATATTACCCCTGTGCACCATGAGGTGAGCGGTACATT         | 714  |
| OY | 746  | GCACTCGCCACCCGTGCAAGGGCTTAAGTTTCCGATCCCGGAGAAAGCCAAATATTAC        | 805  |
| Db | 715  | GCTGTGCCACCCAGTCAAGGCCCTGTGAGATTCGATACCCCGGAAATGCAAAATGCTC        | 774  |
| OY | 806  | AATGTGCACTAGATGATCCCTCTTACAGCATGGTCTTCTGTATGTTCAATGGCTACA         | 865  |
| Db | 775  | AAGTGTGCAACTAGATGATCCCTCTTCTGCAATGGGTGCTGCTGTATGTTCATGGCACCC      | 834  |
| OY | 866  | ACAAATATACAGGCAAGTTCATAGATTGTACACTAACATTCTTCATATCCAACTGTGTAC      | 925  |
| Db | 835  | ACAAATATACAGGCAAGGGGTTCATAGATTGACCCCTTCACCTTCCCAACCAACTGTGTAC     | 894  |
| OY | 926  | TGGGAAGAACCGCGGAAGATCTGTGTTTCACTTTCGCTTCAATATGCGAGTGGCTATC        | 985  |
| Db | 895  | TGGGAAGAACCTGCTCAAAATCTGTGCTTATCTTATCTTATCATGCGCATCTCTATTC        | 954  |
| OY | 986  | ATTACCGTGTGCTATGAGACTGATGCTTGGGCTTCAAGATGTCCGAGTGGCTCTCTGGC       | 1045 |
| Db | 955  | ATTCACGTGTGTGTACGGCTGATGATCTTACAGACTAAAGAGGTTTGCATGTGTATCGGG      | 1014 |
| OY | 1046 | TCCAAAGAAAGACAGGAATCTTGCAGAGATCCACGAGATGTGCTGTGGTGTGGCT           | 1105 |



|   |      |   |      |
|---|------|---|------|
| Db  | 1015 | TCCAAGAAAAGACAGAAATCGCGAGGATCACCCGGATGGTGTGGTTCGGGT           | 1074 |
| Qy  | 1106 | GTGTTCAATCGCTCTGTGGACTGCCATTACATTTACGTATCATTAAGCTTGGTACA      | 1165 |
| Db  | 1075 | GTATTTATCGCTGTGGACCCCCATTCACATCTACGTATCATCAAAAGCGTGTACAG      | 1134 |
| Qy  | 1166 | ATCCCAAGAACTACGTTCCAGACTGTTTCTGGCACTTCGATTCGCTAGTATACACA      | 1225 |
| Db  | 1135 | ATTCGAGAAACACATTTTCAGACCGTTTCTGACACTTCTGCAATTCCTTGGGTTACAG    | 1194 |
| Qy  | 1226 | AACAGCTGCCCTCAACCCAGTCCTTTATGCAATTTCTGGATGAAAACTCAAGATGCTTC   | 1285 |
| Db  | 1195 | AACAGCTGCCCTGAATCCAGTTCTTTACGCCCTTCCTGGATGAAAACTCAAGCATGCTTC  | 1254 |
| Qy  | 1286 | AGAGATGTCGTATCCCAACCTCTCTCCACATTTAGCACACAAAACCTCCACTGGAATTCGT | 1345 |
| Db  | 1255 | AGAGATGTCGTATCCCAACCTCTCTCCACATTTAGCACACAAAACCTCCACTGGAATTCGT | 1314 |
| Qy  | 1346 | CAGAACACTAGAGACACACCCCTCCAGGGCCATATACAGTGGATAGAATATATCAGCTA   | 1405 |
| Db  | 1315 | CAGAACACTAGAGGACATCCCTCCACGGGCTAATACAGTGGATGAACTAACACACAGCTA  | 1374 |
| Qy  | 1406 | GAAATCTGGAAGAGAAACTGCTCCGTTGCCCTAACAGGGTCTCATGCCATTCGGACT     | 1465 |
| Db  | 1375 | GAAATCTGGAAGGACGAAACCTGCTCCATTCGCCCTTAAGTGGTCTCACACATCCAGACCC | 1434 |
| Qy  | 1466 | TCACCAAGCTTAGAAGCCACCATGTAATGTGGAAGCAGGTGCTTCAAGATGTGTAGAG    | 1525 |
| Db  | 1435 | TCGCTAAGCTTAGAGAGCCGCCCATCTACGTGGAATCAAGTTCGCTGAGGGTCTGTGGAG  | 1494 |
| Qy  | 1526 | GCTTAATCTCTAGGAAAGTGCCTGTTTAAAGTATCCAACTCTTTCCTCTGACC         | 1585 |
| Db  | 1495 | GCTCTGATTCCTGTAGAAA---CCATCTGTACTCTGCATTCAAGATCATTCCTCTGCT    | 1554 |
| Qy  | 1586 | ACTCTGCTGTGCACATATAGAG  | 1606 |
| Db  | 1552 | ACTTCACTGTGCACATATAGAG  | 1572 |
| RESULT 8  |      |   |      |
| PCT-US94-10358-1  |      |   |      |
| Sequence 1, Application PC/TUS9410358                             |      |   |      |
| GENERAL INFORMATION:  |      |   |      |
| APPLICANT:  |      |   |      |
| TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND METHODS |      |   |      |
| NUMBER OF SEQUENCES: 17   |      |   |      |
| CORRESPONDENCE ADDRESS:   |      |   |      |
| ADDRESSEE: Arnold, White & Durkee                                 |      |   |      |
| STREET: P. O. Box 4433  |      |   |      |
| CITY: Houston   |      |   |      |
| STATE: Texas  |      |   |      |
| COUNTRY: USA  |      |   |      |
| ZIP: 77210  |      |   |      |
| COMPUTER READABLE FORM:   |      |   |      |
| MEDIUM TYPE: Floppy disk  |      |   |      |
| COMPUTER: IBM PC compatible                                       |      |   |      |
| OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII                             |      |   |      |
| SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25                    |      |   |      |
| CURRENT APPLICATION DATA:   |      |   |      |
| APPLICATION NUMBER: PCT/US94/10358                                |      |   |      |
| FILING DATE: Concurrently herewith                                |      |   |      |
| CLASSIFICATION:   |      |   |      |
| PRIOR APPLICATION DATA:   |      |   |      |
| APPLICATION NUMBER: 08/120.601                                    |      |   |      |
| FILING DATE: 13 SEPTEMBER 1993                                    |      |   |      |
| ATTORNEY/AGENT INFORMATION:                                       |      |   |      |
| NAME: WILSON, MARK B.   |      |   |      |
| REGISTRATION NUMBER: 37,259                                       |      |   |      |
| REFERENCE/DOCKET NUMBER: INDA005P--                               |      |   |      |
| TELECOMMUNICATION INFORMATION:                                    |      |   |      |
| TELEPHONE: (512) 418-3000   |      |   |      |
| TELEFAX: (713) 789-2679   |      |   |      |

| Query Match   | Best Local Similarity | Score                     | No. 123    | 8   | DB     | 5  | Length | 1618 |
|---|-----------------------|---------------------------|------------|-----|--------|----|--------|------|
| Matches 1232  | Conservative          | 0                         | Mismatches | 247 | Indels | 11 | Gaps   |      |
| 69.8%   | 83.7%                 | Pred.                     | No. 3e-290 |     |        |    |        |      |
| TELEX: 79-0924  | 1:                    | SEQUENCE CHARACTERISTICS: |            |     |        |    |        |      |
| LENGTH: 1618 base pairs   |                       | TYPE: nucleic acid        |            |     |        |    |        |      |
| STRANDEDNESS: single  |                       | TOPOLOGY: linear          |            |     |        |    |        |      |
| MOLECULE TYPE: cDNA   |                       | FEATURE:                  |            |     |        |    |        |      |
| NAME/KEY: CDS   |                       | LOCATION: 214..1410       |            |     |        |    |        |      |
| PCT-US94-10358-1  |                       |                           |            |     |        |    |        |      |
| 27 GTGGAGGGGGGCTATACGAGAGAGAAATGTGATGCTACCTCGGTCCTCCGCGCTG            | 86                    |                           |            |     |        |    |        |      |
| 2 GTGGAGGGGGGCTACAGAGAGAGAAATATACAGCGCTCAGA-CGTTCCCTTCTCGCTG          | 60                    |                           |            |     |        |    |        |      |
| 87 ACGCTCTCTCTGTGTCTCAGCCAGAGACTGGTTTCTGTAAACAACAGCAGAG-CTGTGGCA      | 145                   |                           |            |     |        |    |        |      |
| 61 CCGCTCTTCTGTGTCTTCTCACAATGAGGCTGTCCATGTAAACAATCTGACGAGGCTTAGGGA    | 120                   |                           |            |     |        |    |        |      |
| 146 GCGGGAAGAAAGAGGCGGCTGAGAGCCCTTGGAAACCGGAAAAGTCTGAGTCTCTCGGCTG     | 205                   |                           |            |     |        |    |        |      |
| 121 GCTGTAGAGAGAAAGGCTGGGGGCGCGTGGAAACCGGAAAAGTCTGAGTCTCTCAGTATAC     | 180                   |                           |            |     |        |    |        |      |
| 206 CTGCGACAGACGCTGCGCCGCGCCGCTCACTACCATGTGAGACAGCAGCTGCCCGCACAGAC    | 265                   |                           |            |     |        |    |        |      |
| 181 AGCCTCACTAGTCCGAGAGAGGCTTACACACCATGTGACAGAGACACCGCCAGGGAAC        | 240                   |                           |            |     |        |    |        |      |
| 266 GCCACCAATTGACATGATAGCCTTGGCGTACTCAAGTTGCTCCGACAGACCCAGCCCGGT      | 325                   |                           |            |     |        |    |        |      |
| 241 ACCACGACGCTGCTCAGACGCCCTTAGCTCAGGCAAGTTGCTCCCGACGA-----CCTGGC     | 294                   |                           |            |     |        |    |        |      |
| 326 TCCTGGGTCACTTGTCCACTTACATGTGCAACCTGTCCGACCCATGCGGTCCGAACCGC       | 385                   |                           |            |     |        |    |        |      |
| 295 TCCTGGCTCAACTTGTCCACGCTTATGTGCAACACAGTCCGATCCATGCGGTGTGAACCGC     | 354                   |                           |            |     |        |    |        |      |
| 386 ACCGACGTGGGGGGGAGAGACAGCCGTGCTCCGACCGGAGAGTCCGCAATGATCAGC         | 445                   |                           |            |     |        |    |        |      |
| 355 ACCGGGCTTGGGGGAGACAGACGCTGTGCGCTTCCAGACCGGACCGCTTCCATGTGTACACA    | 414                   |                           |            |     |        |    |        |      |
| 446 GCCATCAGGATATGAGCCCTCTACTCCATCGTGTGCGTGTGGGGCTCTTGGAAAATTC        | 505                   |                           |            |     |        |    |        |      |
| 415 GCCATACCATGATGAGCCCTCTACTCTATCGTGTGTGTGTGGGGCTCTTGGAAAATTC        | 474                   |                           |            |     |        |    |        |      |
| 506 CTGGTCACTATGTATGTATTTGTCAAGATACACCAAGATGAGAGACTGCGACCAACATCTACATT | 565                   |                           |            |     |        |    |        |      |
| 475 CTGGTCACTATGTATGTATTTGTCAAGATACACCAAGATGAGAGACTGCGACCAACATCTACATT | 534                   |                           |            |     |        |    |        |      |
| 566 TTCAACCTTGTCTGTGGAGAGTGCCTTAGCGACACAGTACCTCCCTTCCAGAGTGTGAAT      | 625                   |                           |            |     |        |    |        |      |
| 535 TTCAACCTTGTCTGTGGAGAGTGCCTTAGCGACACAGTACCTCCCTTCCAGAGTGTGAAT      | 594                   |                           |            |     |        |    |        |      |
| 626 TACCTAATGGGAACATGGCCATTTGGAACCATCTTTGCAAGATAGTGTCTCCATAGAT        | 685                   |                           |            |     |        |    |        |      |
| 595 TACCTAATGGGAACATGGCCATTTGGAACCATCTTTGCAAGATAGTGTCTCCATAGAT        | 654                   |                           |            |     |        |    |        |      |
| 666 TACCTAATGGGAACATGGCCATTTGGAACCATCTTTGCAAGATAGTGTCTCCATAGAT        | 745                   |                           |            |     |        |    |        |      |
| 655 TACCTAATGGGAACATGGCCATTTGGAACCATCTTTGCAAGATAGTGTCTCCATAGAT        | 714                   |                           |            |     |        |    |        |      |
| 746 GCAGTCTGCGACCCCTGTCAAGGCTTTAGATTTCGTACTCTCCCGAAGTCCGAAAATTAT      | 805                   |                           |            |     |        |    |        |      |
| 715 GCTGTCTGCGACCCCTGTCAAGGCTTTAGATTTCGTACTCTCCCGAAGTCCGAAAATTAT      | 774                   |                           |            |     |        |    |        |      |
| 806 AATGTCTGCACTGGATCTCTCTTCCAGCAGATTTGCTCTCTGTATGTTCATGGCTACA        | 865                   |                           |            |     |        |    |        |      |
| 775 AATGTCTGCACTGGATCTCTCTTCCAGCAGATTTGCTCTCTGTATGTTCATGGCTACA        | 834                   |                           |            |     |        |    |        |      |



|    |      |  |      |
|----|------|--|------|
| Db | 595  | TACCTGATGGGAACATGGCCCTTGGAGACCATTCTCTGCAACATGCTGATCTCAATGAT      | 654  |
| Oy | 666  | TACTATTAACATGTTTCACCAACATATTTACCCCTCTGCACCATGAGTGTGTTGATCGATACAT | 745  |
| Db | 655  | TACTACAACATGTTCAACCAACATATTACCCCTCTGCACCATGAGCGTGGACCGGTACATT    | 714  |
| Oy | 746  | GCACTGTGCCACCCCTGTGCAGAGCCCTTAGATTTCGCTACTGCCCGGAAATGCCAAATTATC  | 805  |
| Db | 715  | GCTGTGTGCCACCCGACAAAGCCCTGGATTTCCTGATCCGCCGAAATGCCAAATTCTCTC     | 774  |
| Oy | 806  | AATGTCGCAACGATGATCCCTCTTAGAGCATTTGGTCTTCCGTAACTGTCATGGCTACA      | 865  |
| Db | 775  | AACGTGTGCACACTGATCTCTCTTCTGCCATCGGTCTGCTGTAACTTATGATGGCAACC      | 834  |
| Oy | 926  | TGGGAAAACCTGCTGGAAGATCTGTGTTTTCATCTTGCCCTTATTTATGCACTGCTATC      | 985  |
| Db | 895  | TGGGAGAAGCTGCTCAAAATCTGTGCTTTATCTTCGCTTTCATCATCCGATCCTCTATC      | 954  |
| Oy | 986  | ATTACCGTGGTATGATGACATGATCTTGGCGCTCAAGAGTCCGAGATGCTCTGCGC         | 1045 |
| Db | 955  | ATCACTGTGTGTACGGCCGTGATGATCTTACGACTCAAGAGGTTTGCGATGCTATCGGCG     | 1014 |
| Oy | 1046 | TCCAAAAGAAAAGCAGAGATCTTCCAAAGATCACAGAGATGTCCTGGTGGTGCTCT         | 1105 |
| Db | 1015 | TCCAAAAGAAAAGCAGAGATCTTCCGCGAGATCACCCGGATGTGCTGTGCTGTGCT         | 1074 |
| Oy | 1106 | GTGTTCATCGTCTGCTGAGCTGCCATTTCACATTTACATGTCATGATTAAGCCTTGGTTACA   | 1165 |
| Db | 1075 | GTAATTATCGTCTGCTGAGCCCTTCCATCCATCATCTACGTATCATCAAGCGCTGATCAG     | 1134 |
| Oy | 1166 | ATCCCAAAACCTAGTTCGACACTGTTTCTTGAGCACTTGTGATTTGCTTGAAGTTACACA     | 1225 |
| Db | 1135 | ATTCACAAACACACATTTCTAGACCGTGTCTCGACATTCCTGATTTGGGTATACAG         | 1194 |
| Oy | 1226 | AACAGCTGCCCTCAACCCGAGCTCTTTATGCAATTTCTGGATGAAGACCTCAAGAGATGCTTC  | 1285 |
| Db | 1195 | AACAGCTGCTGAATCGCATTTCTTTTACGCCCTTCTGTGATGAAGAACTTCAAGCAGTCTTC   | 1254 |
| Oy | 1286 | AGAGAGTTCTGTATCCCAACCTCTTCCAACTTGAGCAACAAACTCGACCTGGAATTCGT      | 1345 |
| Db | 1255 | AGAGAGTTCTGTATCCCAACCTCTGCTCCACGATGGAACAGCAAAACTCCACCTGAGTCTG    | 1314 |
| Oy | 1346 | CAGAACACTAGAGACCAACCCCTCCACGGCCAAATACAGTGGATAGAACATATATCAGCTA    | 1405 |
| Db | 1315 | CAGAACACTAGGAGAACCTCCCTCCACGGGCTAAATACAGTGGATGCAACTAACACACAGCTA  | 1374 |
| Oy | 1406 | GAAATTTGAGAACAGAAACTGTGCTGGTGGCCCTTAACAGGGTCTCATGCAATTCGACCTT    | 1465 |
| Db | 1375 | GAAATTTGAGAGGAGCAAACTGCTCATTTGGCCCTTAACAGGGTCTCAACATCCAGACCC     | 1434 |
| Oy | 1466 | TCACCAAGCTTAGAGGACCAACATGATATGAGGAAGCAGGTTGCTTCAAGATATGTAGAG     | 1525 |
| Db | 1435 | TCGCTAAGCTTAGAGGACCGGCATCTACGTAGGAATACAGTTGCTGTGACAGGTGTGTAGAG   | 1494 |
| Oy | 1526 | GCTCTAATCTCTAGCAAGAGTGCCTTTTAAGTATCCAAACCTCTTCTCTCTGCGC          | 1585 |
| Db | 1495 | GCTCTGCTTCTCAGCAAA---CCATCTGATCTCTGATTCAAAGATCATTTCTCTGCTGCT     | 1551 |
| Oy | 1586 | ACTCTGCTGCAACATTTAGAG  | 1606 |
| Db | 1552 | ACTTCACTCTGCACATGAGAG  | 1572 |

US-387-707-15

Sequence 15, Application US/08387707

Patent No. 6265563

GENERAL INFORMATION:

|   |   |      |  |      |
|---|---|------|--|------|
| D | b | 493  | GTAGTGGGCTCTTTGGAAACTTCCTGCTATGTATGTATGTATAGATATACCAAAATG        | 552  |
| O | y | 542  | AAGACTGCCACCAACATCTACATTTTCACCTTGCTCTGGACAGATCCCTTAGCCACAGT      | 601  |
| D | b | 553  | AAGACTGCCACCAACATCTACATTTTCACCTTGCTCTGGACAGATCCCTTAGCCACTAGC     | 612  |
| O | y | 602  | ACCCGGCCCTTCGAGAGTGAATACCTATATGGGAAACATGGCATTTTGGAAACCATCCCT     | 661  |
| D | b | 613  | ACGCTGCCCCCTTCAGAGTGTAACTACTCTATGGGAACAGGGCCCTTGTGGAAACATCCTC    | 672  |
| O | y | 662  | TGCAGATAGTATCTCCATAGATTACTATACATGTCCACGACATATTTCAACCCCTGTC       | 721  |
| D | b | 673  | TGCAGATAGTATCTCCATAGATTACTATACATGTCCACGACATATTTCAACCCCTGTC       | 732  |
| O | y | 722  | ACCATGATGTGTATCCATATACATTGGCAGTGTGCCACCCCTGTCAAGCCCTTAATTTCCGT   | 781  |
| D | b | 733  | ACCATGATGTGTATCCATATACATTGGCAGTGTGCCACCCCGTCAAGCCCTGTGATTTCCGT   | 792  |
| O | y | 782  | ACTCCGCCAAATGGCAAAATATCAATGTGTGCACGTGATCCCTCTTCACCACTTGGT        | 841  |
| D | b | 793  | ACCCCCCAATTGGCAAAATTTGTCAATGTGTGCACGTGATCCCTCTTCACCACTTGGT       | 852  |
| O | y | 842  | CTTCTCTATATGTTCATAGCTTACACAAATACAGCAAGTTCATATGATTTGACACTA        | 901  |
| D | b | 853  | CTGCCCGTAAATGTTCATAGCTTACACAAATACAGCAGGGGTTCATATATGTACACCTTC     | 912  |
| O | y | 902  | ACATTCCTCATATCCAACTGGTATCTGGGAACCTGCTGAAGTATCTGTTTTCATCTTC       | 961  |
| D | b | 913  | ACGTTCTCTCATCCCACTAGTATCTGGGAACACTGCTCAAAATCTGTCTCTTCATCTTC      | 972  |
| O | y | 962  | GCCTTCATTTATGCCAGTGTCTCATCTATTACCGTGTGCTATGAGACTGATGATCTTGGCCTC  | 1021 |
| D | b | 973  | GCCTTCATCTCATGCCGGCCCTCATCTATCACTGTGTATTAGACTGATGATCTTTCACAGCTC  | 1032 |
| O | y | 1022 | AAGAGTGCCTCCATGCTCTCGTGGCTCCAAAGAAAGACAGGAATCTTGAAGGATTCAC       | 1081 |
| D | b | 1033 | AAGAGTGCCTCCATGCTCTCGTGGCTCCAAAGAAAGACAGGAATCTTGAAGGATTCAC       | 1092 |
| O | y | 1082 | AGGATGT      | 1141 |
| D | b | 1093 | CGGATGGT     | 1152 |
| O | y | 1142 | GTCATCATTAAGCTCTGGTGTACAAATCCCAAGAAATACGTTCCAGACTTTTCTTGGGAC     | 1201 |
| D | b | 1153 | GTCATCATTAAGCTCTGGTGTACAAATCCCAAGAAATACGTTCCAGACTTTTCTTGGGAC     | 1212 |
| O | y | 1202 | TTTCGATTTGCTCTAGGTTTACACAAACAGTGTGCTTACCCAGTCCCTTTATGATTTCTG     | 1261 |
| D | b | 1213 | TTTCGATTTGCTCTAGGTTTACACAAACAGTGTGCTTACCCAGTCCCTTTATGATTTCTG     | 1272 |
| O | y | 1262 | GATGAACATTTCAAGCATGCTTCAGAGATTTGTATGCCAACCTCTTCCACAAATTGAG       | 1321 |
| D | b | 1273 | GATGAACATTTCAAGCATGCTTTTAGAGATTTGTGATGCCAACCTCTTCCACAAATTGAG     | 1332 |
| O | y | 1322 | CAACAAACATCTCACTGCAATTCGCAGCAACACTAGAGACACACCCCTCCAGCCCAATPCA    | 1381 |
| D | b | 1333 | CAGCAAAATCTGCTCCAAATCCGTCAAACACTAGAGGAACACCCCTCCAGCCCTAATPCA     | 1392 |
| O | y | 1382 | GTGATAGAACTAATCATCATCAGCTAGAAAATCTGGAAGACAGAAATCTGCTCCGTTGCCCTA  | 1441 |
| D | b | 1393 | GTGATAGAACTAATCATCATCAGCTAGAAAATCTGGAAGACAGAAATCTGCTCCGTTGCCCTA  | 1452 |
| O | y | 1442 | CAGGCTCTCATGCCATTCGCACTTCCACCAAGCTTGAAGACCACTGATATGTGGAGACA      | 1501 |
| D | b | 1453 | CTGGGCTCCACAGCCATCAACACCTCTGCTAACTTTAGAGGCTGCATCTACTTAACTTGAATCA | 1512 |
| O | y | 1502 | GGTGTCTTCAAGATGTGTAGAGAGGCTCAATTTCTGTAGAAAAGTGGCTGCTTTTAAGTTC    | 1561 |
| D | b | 1513 | GGTGTCTCTCAAGGATTTGTGTGGAGAGGCTCTGTCTTCTGAAAAGCATCTGATCTGCATCT   | 1572 |
| O | y | 1562 | ATCCAACTCTTTCTCTCTGCGCACCTC                                      | 1589 |

| DB                         | 1573  | ATTCAAGCATTCCTCTCTGCGATTTC                                      | 1600               |
|----------------------------|-------|---|--------------------|
| RESULT                     | 11    |   |                    |
|                            |       | US-08-430-286A-1  |                    |
|                            |       | ; Sequence 1, Application US/08430286A                          |                    |
|                            |       | ; Patent No. 6225080  |                    |
|                            |       | GENERAL INFORMATION:  |                    |
|                            |       | APPLICANT: Uhl, George R.                                       |                    |
|                            |       | APPLICANT: Eppier, C. Mark                                      |                    |
|                            |       | APPLICANT: Wang, Jai-Bel  |                    |
|                            |       | TITLE OF INVENTION: Mu-Subtype Opioid Receptor                  |                    |
|                            |       | NUMBER OF SEQUENCES: 14   |                    |
|                            |       | CORRESPONDENCE ADDRESS:   |                    |
|                            |       | ADDRESSEE: Darby & Darby PC                                     |                    |
|                            |       | STREET: 805 Third Avenue  |                    |
|                            |       | CITY: New York  |                    |
|                            |       | STATE: New York   |                    |
|                            |       | COUNTRY: US   |                    |
|                            |       | ZIP: 10022  |                    |
|                            |       | COMPUTER READABLE FORM:   |                    |
|                            |       | MEDIUM TYPE: Floppy disk  |                    |
|                            |       | COMPUTER: IBM PC compatible                                     |                    |
|                            |       | OPERATING SYSTEM: PC-DOS/MS-DOS                                 |                    |
|                            |       | SOFTWARE: Patentin Release #1.0, Version #1.25                  |                    |
|                            |       | CURRENT APPLICATION DATA:                                       |                    |
|                            |       | APPLICATION NUMBER: US/08/430,286A                              |                    |
|                            |       | FILING DATE: 28-APR-1995  |                    |
|                            |       | CLASSIFICATION: 536   |                    |
|                            |       | ATTORNEY/AGENT INFORMATION:                                     |                    |
|                            |       | NAME: Robinson, Joseph R.                                       |                    |
|                            |       | REGISTRATION NUMBER: 33,448                                     |                    |
|                            |       | REFERENCE/DOCKET NUMBER: 0646/1A843-US5                         |                    |
|                            |       | TELECOMMUNICATION INFORMATION:                                  |                    |
|                            |       | TELEPHONE: 212-527-7700   |                    |
|                            |       | TELEFAX: 212-753-6237   |                    |
|                            |       | TELEX: 236687   |                    |
|                            |       | INFORMATION FOR SEQ ID NO: 1:                                   |                    |
|                            |       | SEQUENCE CHARACTERISTICS:                                       |                    |
|                            |       | LENGTH: 2135 base pairs   |                    |
|                            |       | TYPE: nucleic acid  |                    |
|                            |       | STRANDEDNESS: single  |                    |
|                            |       | TOPOLOGY: linear  |                    |
|                            |       | MOLECULE TYPE: CDNA to mRNA                                     |                    |
|                            |       | ORIGINAL SOURCE:  |                    |
|                            |       | ORGANISM: Rattus rattus   |                    |
|                            |       | IMMEDIATE SOURCE:   |                    |
|                            |       | CLONE: mu receptor CDNA   |                    |
|                            |       | US-08-430-286A-1  |                    |
| Query Match                | 64.1% | Score 1031.6;   | DB 4; Length 2135; |
| Best Local Similarity      | 84.7% | Pred. No. 1.3e-265;   |                    |
| Matches 1183; Conservative | 0;    | Mismatches 204;   | Indels 9; Gaps 2;  |
| QY                         | 211   | ACAGGTCGCCCGCCGCGCGCTGACAGTACCATGAGACAGCAGCGTCGCCGCCACAGACGCGAG | 270                |
| DB                         | 3     | ACCTAGTCCGACGACGAGCGCTTCAGACCATGACACGACGACCGGCCAGGAAACACCAG     | 62                 |
| QY                         | 271   | CAATTGCACGTAGTGCCTTGCGGTACTCAAGTTGCTCCCGACGACACCCCGGTTCTCG      | 330                |
| DB                         | 63    | CGACTGCTCAGACCCCTTAGCTCAGGCAAGTTGCTCCCGACCA-----CCTGCTCCTG      | 116                |
| QY                         | 331   | GGTCACTTGTCCCACTTAGATGGCAACCTTCTCCGACCCATGCGGTCCGAACCCGACCGA    | 390                |
| DB                         | 117   | GCTCAACTGTGCCACGCTGATGGCAACCACTCCGATCCAGTCCGATGGAACCCGACCG      | 176                |
| QY                         | 391   | CCTGGCGGAGAGACACCTGTGCGCTCCGACCGGCGAGTCCCTCCATGATCAGCGGCAT      | 450                |
| DB                         | 177   | GCTTGGCGGAGACGACCTGTGCTCCCTCAGACCGGCGACCTTTCATGTGTCACAGCCAT     | 236                |
| QY                         | 451   | CACGATCATGGCCCTCTACTCCATCGTGTGCGGTGGTGGGCGCTCTTGGAAACTTCTG      | 510                |







Thu May 2 11:42:21 2002

us-08-305-518-7.rni

Page 16

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1 APPLICATION NUMBER: US/08/147,592A
2 FILING DATE: 05-NOV-1993
3 CLASSIFICATION: 435
4
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 08/100,694
7 FILING DATE: 30-JUL-1993
8 CLASSIFICATION: 435
9 APPLICATION NUMBER: 08/066,296
10 FILING DATE: 20-MAY-1993
11 CLASSIFICATION: 435
12
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Wilson, Mark B.
15 REGISTRATION NUMBER: 37,259
16 REFERENCE/DOCKET NUMBER: ARCD:105
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: (512) 418-3000
19 TELEFAX: (512) 474-7577
20
21 TELEX: N/A
22
23 INFORMATION FOR SEQ ID NO: 3:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 2272 base pairs
26 TYPE: nucleic acid
27 STRANDEDNESS: single
28 TOPOLOGY: linear
29 MOLECULE TYPE: CDNA
30
31 FEATURE:
32 NAME/KEY: CDS
33 LOCATION: 12..1127
34
35 US-08-147-592A-3

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| Best Local Similarity     | 67.38; | Pred. No. 9.7e-109; |           |              |
| Matches 641; Conservative | 0;     | Mismatches 308;     | Indels 3; | Gaps 1;      |

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| OY | 432 | CTCCTCATATCAGCGCCATCCACAGTATGAGCCCTTACTACATACGTGTCGAGTGGGGC    | 491  |
| Db | 142 | CGTCCCTGCGCCATGCGCATGCGCATCCGCCGCTTACTTACGCTGTGTCCGACATGAGGGC  | 201  |
| OY | 432 | TCCTTCGAAACTCTCCGATCATGTATGTATGTAGATTGCAGATACACCAAGATGAACTGCCA | 551  |
| Db | 202 | TTCTTGGGCAACGTCGTGTCATCTTTTGGATCGTCGGGTACACCAATATGAAGACCGCA    | 261  |
| OY | 552 | CCAACTCTACATTTTCAACCTTGCTCTGGCAATAGCTTAGCCACACATACCCTGCCCT     | 611  |
| Db | 262 | CCAACTCTACATTTTCAATCTGGCTTTGGCTATGCGCTGCGCACACACAGCTGCCCT      | 321  |
| OY | 612 | TCGAGAGTGTAAATTACCTAATGGGAACAATGAGCCATTTGGAAACATCTTTGCAGATAG   | 671  |
| Db | 332 | TCCAGAGGCGCAATACTGTATGGAAACGTGGCCGTTTGGCGAGCTGTGTCAAGGCTG      | 381  |
| OY | 672 | TGATCTCCATGATTTACTATTAACATGTTCACACAGCAATTCACACCCCTGCACACATGAG  | 731  |
| Db | 382 | TGCTCTCCATTTGACTACTACAACTGTTCACATGCACTTTCACCCCTCACATGATGAGG    | 441  |
| OY | 732 | TTGATCGATACATTCAGAGTCTGCGACCCCTTCAGAGCCTTAGATTCTCTACTCCCGAA    | 791  |
| Db | 442 | TGCAACCGTACATTCGTGTGCGCATCTGTCAAAACCCCGAGCTTCGGGACACCGACA      | 501  |
| OY | 792 | ATGCCAAATATTATCAATGTCTGCACACTGATCTCTCTTCAGCCATTTGCTTCTCTGTA    | 851  |
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| OY | 852 | TGTTTATGGGCTAACCAAAATATACAGGCAAGTTCATAGATGTGTATACATACATCTCTC   | 911  |
| Db | 562 | TGCTCATATGGACATGACCCAAACCCCGGAGTGTACAGAGTATGACATGCTCCAGTTCCCA  | 621  |
| OY | 912 | ATCCAACTGTACTGGGAAACCTGCTGAAGATCTGTGTTTCATCTTCGCGCTTCATTA      | 971  |
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| OY | 972 | TGCCAGTGTCTATTATACCGTGTGCTATGAGCTGATCTTGGCGCTCAAGAGTCTC        | 1031 |

|    |      |  |      |
|----|------|--|------|
| Db | 682  | TGGCGATCCATCATCATCAGCGTGTGCTATGAGGCTCATGTCTACTGGGCGCTGGGCAAGCGTGC  | 741  |
| OY | 1032 | GCATGCTCTCTGGGCTCCAAAGAAAGAGACAGCAATCTTGAAAGATCACACAGATGTGCT       | 1091 |
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| Db | 742  | GTCGTGCTCCGGTTCACAGAGAAAGAGACCGGCGAGCTCCGGCGCATACAGGCACTGTGTC      | 801  |
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|    |      |  |      |
| Db | 802  | TGGTGGTGGTGGGCGCTTGTGTGTGTGTGTGGGCGGCCATTCACATTTGTGTCATTCGCT       | 861  |
| OY | 1152 | AAGCTTTGGTTACATC---CCAGAAACTACGTTCCAGACTTTTCTTGAGCACTTGTCA         | 1208 |
|    |      |  |      |
| Db | 862  | GGAGCGCTGGTGGACATCAATCAATCGGCGGAGCCACTGTGTGTGGCGGACTGCACCTGTGCA    | 921  |
| OY | 1209 | TTTGCTAGGTTACACAAACAGCTGCCCTCAACCCAGCTCTTTATGCAATTTCTGATGAAA       | 1268 |
|    |      |  |      |
| Db | 922  | TTTGCGCTGGGCTTAGGCCAACAGCAGCGCTCAACCCGGTCTCTACGCCCTCCGAGCAGGA      | 981  |
| OY | 1269 | ACTTCAACAGATGCTTTCAGAGAGATTCTGTATTCCCAAACCTCTTTCCAAACATTTAGCAACAAA | 1328 |
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| OY | 1329 | ACTCCACTCGAATTCGTGCAGACACATCAGAGACACACCCCTCCAGCGCAATAGC            | 1380 |
|    |      |  |      |
| Db | 1042 | GTTCTCGCTGCTCCCGCGCAGGCCACCAACGCGGTGAGGTGTCACTGCTGCAC              | 1093 |

Search completed: May 1, 2002, 22:15:36  
Job time: 4258 sec







GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2002, 18:48:26 ; Search time 1541.38 Seconds

(without alignments)  
11224.165 Million cell updates/sec

Title: US-08-305-518-7

Perfect score: 1610  
Sequence: 1 CGGATGACCCCTGTGAACT.....GCTCTGACATTAGAGGCCG 1610

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: em\_estfun: \*  
2: em\_esthum: \*  
3: em\_estlin: \*  
4: em\_estom: \*  
5: em\_estpl: \*  
6: em\_estba: \*  
7: em\_estro: \*  
8: em\_estov: \*  
9: em\_hlc: \*  
10: gb\_est1: \*  
11: gb\_est2: \*  
12: gb\_hlc: \*  
13: gb\_gss: \*  
14: em\_gss\_fun: \*  
15: em\_gss\_hum: \*  
16: em\_gss\_inv: \*  
17: em\_gss\_pln: \*  
18: em\_gss\_pro: \*  
19: em\_gss\_rod: \*  
20: em\_gss\_vrt: \*  
21: em\_gss\_other: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| C 1        | 323.6 | 20.1        | 520    | 13    | B82759 RPC11-17K2  |
| C 2        | 322.2 | 20.0        | 1053   | 13    | CNS04C2T           |
| C 3        | 227   | 14.1        | 525    | 13    | A0767579 HS_3206.A |
| C 4        | 222.2 | 13.8        | 389    | 10    | BE649947 UI-M-BH3- |
| C 5        | 213.8 | 13.3        | 836    | 13    | CNS02261           |
| C 6        | 211   | 13.1        | 877    | 13    | CNS02SC2           |
| C 7        | 191   | 11.9        | 842    | 13    | CNS02SKU           |
| C 8        | 186.8 | 11.6        | 710    | 13    | CNS012MG           |
| C 9        | 184.2 | 11.4        | 433    | 10    | AM489031           |
| C 10       | 158.6 | 9.9         | 927    | 13    | CNS04RP2           |
| C 11       | 158.2 | 9.8         | 881    | 13    | CNS03JCN           |
| C 12       | 155.4 | 9.7         | 654    | 10    | AM373832           |

|      |       |     |      |    |          |                    |
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| 13   | 153.8 | 9.6 | 702  | 13 | A2966515 | AM0237H04          |
| 14   | 144.8 | 9.0 | 530  | 11 | BF193020 | BF193020 24449 MA  |
| C 15 | 137.6 | 8.5 | 427  | 10 | AM047705 | AM047705 UI-M-BH1- |
| C 16 | 136.4 | 8.5 | 245  | 13 | AQ488720 | AQ488720 RPC1-11-2 |
| 17   | 130.4 | 8.1 | 642  | 10 | BE252309 | BE252309 601114162 |
| 18   | 127.4 | 7.9 | 741  | 11 | BI224313 | BI224313 602940621 |
| 19   | 125.6 | 7.8 | 888  | 11 | BF676176 | BF676176 602084171 |
| 20   | 124   | 7.7 | 546  | 13 | A2226406 | A2226406 RPC1-23-8 |
| 21   | 124   | 7.7 | 904  | 11 | BG329444 | BG329444 602429002 |
| 22   | 123.8 | 7.7 | 937  | 13 | CNS03SG  | AL243385 Tetraodon |
| 23   | 122   | 7.6 | 530  | 11 | BF073470 | BF073470 220178 MA |
| C 24 | 117.2 | 7.3 | 995  | 13 | CNS04ROE | AL304223 Tetraodon |
| 25   | 116.2 | 7.2 | 832  | 10 | AL336712 | AL336712 AL336712  |
| 26   | 115.4 | 7.0 | 183  | 11 | R81583   | R81583 y104b04.t1  |
| 27   | 112.2 | 7.0 | 638  | 10 | AM919332 | AM919332 EST350636 |
| 28   | 108   | 6.7 | 656  | 10 | AL119185 | AL119185 DKFZP761N |
| 29   | 107.2 | 6.7 | 534  | 10 | AM652898 | AM652898 101337 MA |
| C 30 | 105.6 | 6.6 | 563  | 13 | A2357931 | A2357931 1M0099P13 |
| C 31 | 98.2  | 6.1 | 794  | 13 | CNS01WC1 | AL170218 Tetraodon |
| C 32 | 98    | 6.1 | 697  | 11 | BG471950 | BG471950 602512853 |
| C 33 | 92.6  | 5.8 | 992  | 13 | CNS022ZG | AL221605 Tetraodon |
| C 34 | 90.8  | 5.6 | 606  | 11 | BG025021 | BG025021 602276041 |
| C 35 | 90.8  | 5.6 | 844  | 13 | CNS03CLX | AL237966 Tetraodon |
| 36   | 89    | 5.5 | 153  | 11 | R31984   | R31984 yh62c10.t1  |
| 37   | 88.6  | 5.5 | 546  | 11 | BG552112 | BG552112 dQ17a03.Y |
| 38   | 88    | 5.5 | 213  | 10 | BE388668 | BE388668 BB588668  |
| C 39 | 87    | 5.4 | 549  | 11 | BE38149  | BE38149 MR3-TN004  |
| C 40 | 87    | 5.4 | 954  | 10 | AL556152 | AL556152 RST1196.A |
| 41   | 86.6  | 5.4 | 884  | 11 | BG182330 | BG182330 RST1196.A |
| 42   | 84.4  | 5.2 | 789  | 11 | BG205056 | BG205056 RST24475  |
| 43   | 83.2  | 5.1 | 781  | 11 | BG681003 | BG681003 602628822 |
| 44   | 82    | 5.1 | 1045 | 11 | BG404113 | BG404113 602420022 |
| C 45 | 80.4  | 5.0 | 901  | 13 | CNS01SK5 | AL165326 Tetraodon |

#### ALIGNMENTS

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LOCUS  
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DNA sequence.  
B82759  
B82759.1 GI:2869782  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (Bases 1 to 520)  
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,  
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and  
Venter,J.C.  
Use of BAC End Sequences for Sequence-Ready Map Building (1998)  
Unpublished (1998)  
Other GSSs: RPC11-17K2.TVB  
CONTACT: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdadams@tigr.org  
Clones are derived from the human BAC library RPC1-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.bufileo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.bufileo.edu/ordering) or from  
Research Genetics (info@resgen.com). BAC end search page:  
http://www.tigr.org/cdb/humgen/bac\_end\_search/bac\_end\_search.html  
Seq primer: SP6  
Class: BAC ends.

#### FEATURES

Location/Qualifiers

[illegible]

| AUTHORS                   | Genoscope.   |
|---------------------------|--|
| TITLE                     | Direct Submission  |
| JOURNAL                   | Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases  |
| COMMENT                   | This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigriviridis genome. For more information, please take a look at <a href="http://www.genoscope.cns.fr/Tetraodon">http://www.genoscope.cns.fr/Tetraodon</a> . |
| FEATURES                  | <p>source</p> <p>location/Qualifiers</p> <p>1..1053</p> <p>/organism="Tetraodon nigriviridis"</p> <p>/db_xref="taxon:99883"</p> <p>/clone="098B06"</p> <p>/clone_1lb="G"</p> <p>/note="Genoscope sequence ID : C08G098DA03SP1-end ; PUC-ori"</p>                                     |
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| 527                       | AGATACACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 586  |
| 582                       | AGGTACACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 581  |
| 587                       | GGCTTAGCCACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 586   |
| 922                       | GCTTAGCCACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 863  |
| 647                       | TTTGGACCAATCTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 706   |
| 862                       | TTTGGACCAATCTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 803   |
| 707                       | ATATTCACCAATCTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 763  |
| 802                       | ATCTTCACCAATCTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 743  |
| 764                       | AAGGCTTAGATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 823  |
| 742                       | CGGGGCGTGAAGATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 683   |
| 824                       | CTCTCTTCAAGCATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 870   |
| 682                       | CTCTCTTCAAGCATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 623   |
| 871                       | -----ATA 873   |
| 622                       | GGTAGTACGAGATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 563  |
| 874                       | CAGGCAAGTTCATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 933  |
| 562                       | CCCGCAGGCAAGTTCATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 503  |
| 934                       | CCTGCTGAAGATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 993   |
| 502                       | GACCATGAAGATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 443   |
| 994                       | GTCATGAGATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 1053  |
| 442                       | CTGTACAGGATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 384  |
| 1054                      | AAAGCAAGATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 1113  |
| 383                       | GAAGCAAGATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 324   |
| 1114                      | CGTGTGAGATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 1173  |
| 323                       | CGTGTGAGATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 264   |
| 1174                      | AATTAAGATTTTGGACCAAGATGAAGAGCTGCACCAACATCTACATTTTCACCTTGTCTGTGCAGAT 1230   |

| Db                    | 1263   | CAAGAACCTGCTGGTGGATTGGACAGCTGGACACTGTGCATCGCGCTGGGCTACATGAACAG | 204         |
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| Db                    | 203  | CAGCTGTAACCGCGGCTCTACGCTCTTCCTGGACGAGAATCTCAAAAGCTGTTCAGGGA    | 144         |
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| DEFINITION            | HS_3206_A1_E05_T77C CIT Approved Human Genomic Sperm Library D Homo  |  |             |
| ACCESSION             | A0767579   |  |             |
| VERSION               | A0767579.1   | GI:5645695   |             |
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| SOURCE                | human.   |  |             |
| ORGANISM              | Homo sapiens   |  |             |
| REFERENCE             | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  |  |             |
| AUTHORS               | 1 (bases 1 to 525)<br>Mahaitas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.   |  |             |
| TITLE                 | Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome   |  |             |
| JOURNAL               | Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  |  |             |
| MEDLINE               | 99380589   |  |             |
| COMMENT               | Contact: Mahaitas GG, Wallace JC, Hood L<br>High Throughput Sequencing Center<br>University of Washington<br>401 Queen Anne Avenue North, Seattle, WA 98109, USA<br>Tel: (206) 616-3618<br>Fax: (206) 616-3887<br>Email: jwallace@u.washington.edu<br>Clones may be purchased from Research Genetics (info@resgen.com).<br>BAC end Web Server: http://www.htsc.washington.edu<br>Plate: 3206 row: 1 column: 9<br>Seq primer: T7<br>Class: BAC ends<br>High quality sequence stop: 525. |  |             |
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|                       | /clone_lib="CIT Approved Human Genomic Sperm Library D"  |  |             |
|                       | /sex="male"  |  |             |
|                       | /note="Organ: sperm; Vector: pbelBAC11; BAC Clones in E-Coli DH10B"  |  |             |
| BASE COUNT            | 123 a 139 c 126 g 133 t  | 4 others   |             |
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| Query Match           | 14.1%:   | Score 227:   | DB 13:      |
| Best Local Similarity | 81.4%:   | Pred. No. 9.3e-50:   | Length 525: |
| Matches 263:          | Conservative 0:  | Mismatches 60:   | Indels 0:   |
|                       |  | Gaps 0:  |             |
| OY                    | 216  | GTGGCCGCCCGCCCTCAGTACATGAGCAGCAGCGCTGCCCCCAGCAGACGACCAATT      | 275         |
| Db                    | 521  | GTGGCAGCCAGACGGCTCAACCTATGACAGCAGCAAGCGTGTCAATTGAACGAGTAATAT   | 462         |
| OY                    | 276  | GCACGTGATGCTTGGCGGTACTCACTGCTGCCAGCAGCAGCCCGGTTCTTGAGTCA       | 335         |
| Db                    | 461  | GAAATGATGCTTACGTAACCTCAAGTTGTCTCCCAAGCACTACCAACGCGTTTCTTGATCA  | 402         |
| OY                    | 336  | ACTTGTCCACTTATATGGCAACCTGTCCGACCACTGGGTCCGAACGACGACGACCTGG     | 395         |
| Db                    | 401  | ACTTGTCCACTTATATGGCAACAGTGTCTTACCACTGGCGTAGAACGCGCCGTCGTGG     | 342         |

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| OY         | 396  | GGGGAGAGACAGCCTGTGGCCCTCGACCGGACAGTCCCATATATCACGGCATATCAAGA | 455                     |
|            |  |   |                         |
| Db         | 341  | GAGGAGAGACAGCTTGTGCTTCGGACAGGACAGTCCCATATATCACGGCATATCAAGA  | 282                     |
| OY         | 456  | TCATGCGCCCTCTACTCCATGCTGTGCTGTGGGGGCTCTTGGAAACTTCTGCTGATGT  | 515                     |
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| Db         | 281  | TCATGCGCCCTGTACTCCATGCTGTGCGGGGTGGGCTCTTGGAAACTTACTGTCATGT  | 222                     |
| OY         | 516  | ATGTGATGTTCAGATATACACCAAG                                   | 538                     |
|            |  |   |                         |
| Db         | 221  | ATGTGATGTTCAGATATACCAAG                                     | 199                     |
| RESULT     | 4  |   |                         |
| BE649947   |  |   |                         |
| LOCUS      |  |   |                         |
| DEFINITION | BE649947   | 389 bp  | mRNA                    |
| ACCESSION  | U1-M-BH3-asd-d-09-0-U1.r1  | NIH_BMAP_M_S4   | Mus musculus cDNA clone |
| VERSION    | BE649947   |   |                         |
| KEYWORDS   | BE649947.1   | GI:9975771  |                         |
| SOURCE     | EST.   |   |                         |
| ORGANISM   | house mouse.   |   |                         |
|            | Mus musculus   |   |                         |
|            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |   |                         |
| REFERENCE  | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |   |                         |
| AUTHORS    | 1 (bases 1 to 389)   |   |                         |
| TITLE      | Bonaldo,M.F., Lennon,G. and Soares,M.B.                            |   |                         |
|            | Normalization and subtraction: two approaches to facilitate gene   |   |                         |
|            | discovery  |   |                         |
| JOURNAL    | Genome Res.  | 6 (9),  | 791-806 (1996)          |
| MEDLINE    | 9704447  |   |                         |
| COMMENT    |  |   |                         |
|            | Contact: Chln, H   |   |                         |
|            | National Institute of Mental Health                                |   |                         |
|            | 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD          |   |                         |
|            | 20892-9643, USA  |   |                         |
|            | Tel: 301 443 1706  |   |                         |
|            | Fax: 301 443 9890  |   |                         |
|            | Email: M5ST@mail.nih.gov   |   |                         |
|            | cDNA library preparation: M.B. Soares Lab Clone distribution:      |   |                         |
|            | Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It |   |                         |
|            | should be noted that Bento Soares is generating a small number of  |   |                         |
|            | additional specialized non-redundant arrays of BMAP cDNAs whose    |   |                         |
|            | availability will be considered under appropriate and limited      |   |                         |
|            | collaborative arrangements   |   |                         |
|            | Seq primer: M13 Reverse.   |   |                         |
| FEATURES   |  |   |                         |
| source     | Location/Qualifiers  |   |                         |
|            | 1..389   |   |                         |
|            | /organism="Mus musculus"   |   |                         |
|            | /strain="C57BL/6J"   |   |                         |
|            | /db_xref="taxon:10090"   |   |                         |
|            | /clone="U1-M-BH3-asd-d-09-0-U1"                                    |   |                         |
|            | /clone_lib="NIH_BMAP_M_S4"   |   |                         |
|            | /dev_stage="27-32 days"  |   |                         |
|            | /lab_host="DHI0B (Life Technologies)"                              |   |                         |
|            | /note="Vector: pT73D-Pac (Pharmacia) with a modified               |   |                         |
|            | polylinker. Site 1: Not I; Site 2: Eco RI; The                     |   |                         |
|            | NIH_BMAP_M_S4 library is a subtracted library of a series          |   |                         |
|            | ultimately derived from a mixture of individually tagged           |   |                         |
|            | normalized libraries from ten regions of the mouse brain           |   |                         |
|            | (cerebellum, brain stems, olfactory bulbs, hypothalamus,           |   |                         |
|            | cortex, amygdala, basal ganglia, pineal gland, striatum,           |   |                         |
|            | hippocampus) after a series of subtractions to reduce the          |   |                         |
|            | representation of cDNAs from which ESTs had already been           |   |                         |
|            | generated. The following serially subtracted libraries             |   |                         |
|            | were generated in this process: NIH_BMAP_M_S4,                     |   |                         |
|            | NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,                 |   |                         |
|            | NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library               |   |                         |
|            | (NIH_BMAP_M_S4) was constructed as follows: PCR amplified          |   |                         |
|            | cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and            |   |                         |
|            | NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived         |   |                         |
|            | was used as a driver in a hybridization with a pool of             |   |                         |
|            | the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1          |   |                         |
|            | libraries in the form of single-stranded circles. The              |   |                         |



| TITLE   | JOURNAL   | REFERENCE  | AUTHORS   | TITLE   | JOURNAL             | COMMENT           |
|---|---|--|---|---|---------------------|-------------------|
| Saurin,W. and Weissenhach,J.                              | Human gene number estimate provided by genome wide analysis using   | Tetraodon nigroviridis DNA sequence                              | Unpublished   | 3 (bases 1 to 877)                                  | Genoscope.          | Direct Submission |
| Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases | This sequence is a single read and was generated as part of a large | scale clone-end sequencing project of the Tetraodon nigroviridis | genome. For more information, please take a look at | http://www.genoscope.cns.fr/tetraodon.              | Location/Qualifiers | 1..877            |
| /organism="Tetraodon nigroviridis"                        | /db_xref="taxon:99883"  | /clone="161H06"  | /clone_11b="G"                                      | /note="Genoscope sequence ID : C0AG161DD03SP1-end ; | PUC-Or1"            |                   |
| BASE COUNT  | 201 a   | 249 c  | 214 g   | 197 t   | 16 others           |                   |
| ORIGIN  |   |  |   |   |                     |                   |
| Query Match   | 13.1%   | Score 211;   | DB 13;  | Length 877;   |                     |                   |
| Best Local Similarity                                     | 74.2%;  | Pred. No. 2.1e-45;   |   |   |                     |                   |
| Matches 262;  | Conservative 3;   | Mismatches 88;   | Indels 0;   | Gaps 0;   |                     |                   |
| 527   | AGATACACCAGATGACACACCTGCCACCAACATCTCATTTTCAACCTTGCTTGACAGAT         | 586  |   |   |                     |                   |
| 348   | AGGTACCCAGATGATGACGCGCCACCAACATCTCATTTTCAACCTTGCTTGACAGAT           | 407  |   |   |                     |                   |
| 587   | GCCTTAGCCACAGTACCTGCTTCCAGAGTGAATTAACCTATGGAGCATGGCCA               | 646  |   |   |                     |                   |
| 408   | GCTTAGCCACAGACACCTCCCTCCATCCAGACGGCCAAAGTACCTATGACACGCGTGG          | 467  |   |   |                     |                   |
| 647   | TTTGAACCATCTTTCGACAGATAGTATCTTCATAGATTACTATTAACATGTTCCAGAC          | 706  |   |   |                     |                   |
| 468   | TTGCGGAGCTGCTGTGCAAACTGGTCATCGCATTTGACTACTACAAATGTTCCAGAC           | 527  |   |   |                     |                   |
| 707   | ATATTCACCCCTCTGCACACATGATGATGATGATGATGATGATGATGATGATGATGAT          | 766  |   |   |                     |                   |
| 528   | ATCTTCACGCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT          | 587  |   |   |                     |                   |
| 767   | GCCTTAGATTTTCCGATCTCCCGAAATGCGAAATTTATCATGTTGCAACTGATCTCTC          | 826  |   |   |                     |                   |
| 588   | GCGCGGAGCTTCCGACACACCGCCCAAGGCGAAATCATCATCATGTTTATCTGATCTC          | 647  |   |   |                     |                   |
| 827   | TCTTCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT          | 879  |   |   |                     |                   |
| 648   | TCTTCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT          | 700  |   |   |                     |                   |
| RESULT 7  | CNS02SKU/c  |  |   |   |                     |                   |
| LOCUS   | CNS02SKU  | 842 bp   | DNA   | GSS   | 15-MAY-2000         |                   |
| DEFINITION  | Tetraodon nigroviridis genome survey sequence T7 end of clone       | 161E18 of library G from Tetraodon nigroviridis, genomic survey  | sequence.   |   |                     |                   |
| ACCESSION   | AL212007.1  | GI:7870826   |   |   |                     |                   |
| KEYWORDS  | GSS: genome survey sequence.  |  |   |   |                     |                   |
| SOURCE  | Tetraodon nigroviridis.   |  |   |   |                     |                   |
| ORGANISM  | Tetraodon nigroviridis  |  |   |   |                     |                   |
| REFERENCE   | Roeest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  |  |   |   |                     |                   |
| AUTHORS   | Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and       |  |   |   |                     |                   |
| TITLE   | Weissenbach,J.  |  |   |   |                     |                   |
|   | Characterization and repeat analysis of the compact genome of the   |  |   |   |                     |                   |

[illegible]











MEDLINE 97044477  
Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: MEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag served to identify it as a clone from the normalized cerebellum library cDNA library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.  
Seq primer: M13 Forward  
POLYA=yes.

FEATURES  
source location/Qualifiers

1..427  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="01-M-BH1-alo-f-04-0-01"  
/clone\_1id="NIH\_BMAP\_M\_S2"  
/dev\_stage="27-32 days"  
/lab\_host="DH10B (Life Technologies)"  
/note="vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; The NIH\_BMAP\_M\_S2 library is a subtracted library derived from NIH\_BMAP\_M\_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH\_BMAP\_M\_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.  
TAG\_LIB=NIH\_BMAP\_M\_S2  
TAG\_TISSUE=cerebellum  
TAG\_SEQ=GACTC

BASE COUNT 119 a 104 c 107 g 97 t  
ORIGIN

Query Match 8.5%; Score 137.6; DB 10; Length 427;  
Best Local Similarity 59.9%; Pred. No. 6.1e-26;  
Matches 230; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

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OY 628 CCTAATGGAGACATGGCCATTGGACCATCCCTTGCAAGATAGATCCCATAGATTA 687
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Db 413 CCTGTGGGCTTATGGCCATTGGCAATGCACTGTGCAAGCGTCATTGATTCGAATA 354
OY 688 CTATACATGTTTACACAGCATATTCACCCCTGACACCATGAGTGTGATCATATGC 747
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Db 353 CTACACATGTTTACACAGCATTTCACTTACATGATGATGATGAGACCTTATGTAGC 294
OY 748 AGTCTGCCACCCCTTCAAGCCCTTAGATTTCCGTAATCCCGAAATGCCAAATTAACA 807
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Db 293 TATCTGCCACCCCTTATCCGCTTGATGTTGACATATCCAGTAAGCCACGCGCTTAA 234
OY 808 TGCTGCAACGATCCCTCTTCATGATGATGATGATGATGATGATGATGATGATGATG 867
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Db 233 TGTGGCCATATGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 174
OY 868 AAATACAGGCAAGGTTCCATAGATTTACATACATTTCTTCATCCCAACCTGTACTG 927
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OY 928 GGAAGACCTGCTGAAGATGCTGTTTCACTTCGCTTCAATATGCAAGTGCATCAT 987
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